

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:16:59 ; Search time 194 Seconds  
(without alignments)  
322.880 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725  
Sequence: 1 AVTKPRYMOMREIWSSTSTL.....HQLSHRLPMAENGRDGYL 137

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq.8: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003s: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*  
10: geneseqp2006s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	725	100.0	137	8	ADRO5215 Human ino
2	725	100.0	604	5	ABB09774 Amino aci
3	725	100.0	604	5	ABB09784 Amino aci
4	725	100.0	660	5	AAE16280 Human kin
5	725	100.0	683	5	ABU65211 Human NOV
6	725	100.0	683	8	ADN62073 Human nov
7	725	100.0	683	9	AE887638 Human ino
8	725	100.0	687	4	AA41393 Human pol
9	725	100.0	711	4	AA439607 Human pol
10	504	69.5	461	5	ABB09772 Amino aci
11	504	69.5	461	8	AD044008 Amino aci
12	504	69.5	461	9	AE887636 Amino aci
13	504	69.5	477	5	ABB09782 Amino aci
14	493	68.0	472	5	ABB09773 Amino aci
15	493	68.0	472	5	ABB09773 Amino aci
16	493	68.0	798	4	AAE04364 Human kin
17	493	68.0	946	9	AE887637 Human ino
18	482	66.5	1192	8	ADRA0445 Mouse ino
19	464	64.0	1339	5	ABG65653 Human bre
20	403.5	55.7	382	4	ABBS8311 Drosophila
21	403.5	55.7	669	4	ABB09771 Amino aci
22	403.5	55.7	669	5	ABB09781 Amino aci
23	382.5	52.8	316	5	AAE26203 Maize ino

24	259.5	35.8	441	5	ABB09770 Amino aci
25	259.5	35.8	441	5	ABB09780 Amino aci
26	145	20.0	71	8	ABO56198 Human gen
27	83	11.4	1051	8	ADT66570 Rat Lutzp
28	81.5	11.2	325	7	ADU69714 Human hea
29	80.5	11.1	349	8	ADN17522 Bacterial
30	79.5	11.0	248	3	AA64592 Arabidops
31	79.5	11.0	281	9	ADX84866 Arabidops
32	79.5	11.0	286	9	ADX84903 Arabidops
33	79.5	11.0	286	9	ADX84882 Arabidops
34	79.5	11.0	293	9	ADX84864 Arabidops
35	79.5	11.0	300	3	AA64591 Arabidops
36	79.5	11.0	300	9	ADX84881 Arabidops
37	79.5	11.0	300	9	ADX84859 Arabidops
38	79.5	11.0	300	9	ADX84880 Arabidops
39	79.5	11.0	330	3	AA64590 Arabidops
40	78.5	10.8	1067	8	ADT66572 Rat Lutzp
41	78	10.8	279	5	AAE26197 Soybean l
42	77	10.6	298	7	ADM25727 Hyperther
43	75.5	10.4	977	5	ABG97350 Human CGD
44	75	10.3	317	8	ADX84855 Plant ful
45	75	10.3	455	8	ADX73267 Plant ful

#### ALIGNMENTS

RESULT 1  
ID ADR05215 standard; protein; 137 AA.  
XX  
AC ADR05215;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
XX Human inositol 1,4,5-triphosphate 3-kinase C (ITPKC) protein.  
XX  
DE  
XX  
KW apoptosis; cytosolic; antiinflammatory; antiasthmatic; respiratory;  
KW antineoplastic; antidiabetic; gynaecological; cardiac; vasotropic;  
KW antiproliferative; anticancer; autolysosomal; immunosuppressive;  
KW neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory;  
KW asthma; chronic obstructive pulmonary disease; cystic fibrosis;  
KW rheumatoid arthritis; acute respiratory distress syndrome; preclampsia;  
KW myocardial ischemia; reperfusion injury; psoriasis; bronchiolitis;  
KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; human;  
KW enzyme; inositol 1,4,5-triphosphate 3-kinase C; ITPKC.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN WO2004065959-A2.  
XX  
PD 05-AUG-2004.  
XX  
XX 23-JAN-2004; 2004WO-GB000271.  
XX  
PF 23-JAN-2003; 2003GB-00001566.  
XX  
PR 25-MAR-2003; 2003US-0457533P.  
XX  
PA (EIRX-) EIRX THERAPEUTICS LTD.  
XX  
PI Seery L, Hayes I, Murphy F;  
XX  
XX WPI, 2004-593556/57.  
XX  
DR N-PSDB; ADR05216.  
XX  
PT Identifying a modulator of apoptosis-associated polypeptide function,  
PT useful for treating e.g., cancer, comprises incubating a sample  
PT containing an apoptosis-associated polypeptide and a candidate agent to  
PT permit binding.  
XX  
PS Claim 1; Page; 230pp; English.  
XX  
XX The invention relates to a novel method for identifying an agent that

modulates the function of an apoptosis-associated polypeptide, particularly a kinase or GPCR (G-protein-coupled receptor). The method comprises providing a sample containing an apoptosis-associated polypeptide and a candidate agent and incubating under conditions to permit binding of the candidate agent to the polypeptide, measuring the binding and comparing it with the binding of the polypeptide to a control agent known not to bind to the polypeptide. The method of the invention has cytostatic, antiinflammatory, antiaesthetic, respiratory, antirheumatic, antitachytic, gynaecological, cardiant, vasotropic, antiproliferic, anticancer, gastroenteric, immunosuppressive and neuroprotective applications. The method and molecules may be useful for treating a disease or condition characterised by abnormal apoptosis in mammalian tissue, particularly cancer, such as small cell lung cancer, cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast, leukaemias, sarcomas and myelomas. Furthermore, autoimmune, neurodegenerative and inflammatory conditions may be treated, including asthma, chronic obstructive pulmonary disease, cystic fibrosis, rheumatoid arthritis, acute respiratory distress syndrome, preclampsia, myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis, Crohn's disease, ulcerative colitis and inflammatory bowel disease. The current sequence is that of a human apoptosis-associated protein of the invention which was used during siRNA (small interfering RNA)-mediated gene silencing.

XX Sequence 137 AA;  
SQ

Query Match	100.0%;	Score 725;	DB 8;	Length 137;
Best Local Similarity	100.0%;	Pred. No. 6.3e-75;		
Matches 137; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 AATKRNRVQMRETMSTSTLGRIRIEGKKADGTCNTNPFKTKQALBQVTKLBEFVVDGHH 60

Db 1 AATKRRVQMRETMSTSTLGRIRIEGKKADGTCNTNPFKTKQALBQVTKLBEFVVDGHH 60

QY 61 ILQKRVACIEEUREALEISPPFRTTHVWSSLLFVMDHTGLACVMMIDPKTALDPDQT 120

Db 61 ILQKRVACIEEUREALEISPPFRTTHVWSSLLFVMDHTGLACVMMIDPKTALDPDQT 120

QY 121 LSHRLPMAGNREDGYL 137

Db 121 LSHRLPMAGNREDGYL 137

RESULT 2  
ABB09774

AC ABB09774;

DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-C.

KM IP3 kinase: inositol-1,4,5-trisphosphate kinase; enzyme; oxidative stress  
 KM endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
 KM chronic infection; arthritis; cancer; cystic fibrosis;  
 KM Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KM DMPK1; DMPK2.

**Homo sapiens.**

PN FR2813612-A1.

08-MAR-2002. PD

07-SEP-2000; 2000FR-00011397.

07-SEP-2000; 2000FR-00011397.

PA (CNRS ) CNRS CENT NAT RECH SCI.

Tricoire H, Monnier V, Pret AM, Cabet DE, Brissard J, Vandurka P;

XX WPI; 2002-260343/31.  
DR N-PSDB; ABL56446.  
DR

PT New proteins with inositol-triphosphate kinase activity, useful e.g. for treating oxidative stress and neurodegeneration.

PS Claim 4; Fig 5; 69pp; French.

The present sequence represents inositol-1,4,5-trisphosphate 3 (IP3) kinase-C protein. The specification also describes Drosophila IP3 kinase proteins, designated DIPK1 and DIPK2. This protein has IP3 (inositol-1,4,5-trisphosphate) kinase activity. The specification describes the use of IP3 kinase proteins to prepare compositions for treating diseases associated with oxidative stress, stress of the endoplasmic reticulum or neurodegeneration, particularly of the retina. Overexpression of IP3 kinase protects cells against the damaging effects of free radicals without altering free radical homeostasis within the cell. The IP3 proteins are used for treating disorders associated with oxidative stress, stress on the endoplasmic reticulum and neurodegeneration, particularly chronic infection (such as athlitis and some forms of cancer), cystic fibrosis; Alzheimer's and Huntington's diseases, and pigmentary retinopathy. Transgenic animals that lack the gene for IP3 kinase proteins are used to identify phenotypic alterations associated with loss of this gene

**SQ** Sequence 604 AA;

Query Match	100.0%	Score 725;	DB 5;	Length 604;
Best Local Similarity	100.0%	Pred. No. 4.9e-74;		
Matches 137; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

### RESULT 3

ID ABB09784 standard; protein; 604 AA.

AC ABB09784;

DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-C.

KW IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
 KW endoplasmic reticulum stress; neurodegeneration; retina, free radical,  
 KW chronic infection; arthritis; cancer; cystic fibrosis;  
 KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KW DIP3K1; DIP3K2.

**Homo sapiens.**

PN WO200220742-A1

14-MAR-2002.

PF 31-AUG-2001; 2001WO-FR002708.

PR 07-SEP-2000; 2000FR-00011397.

PA (CNRS ) CENT NAT RECH SCI.

12

XX	WO200196547-A2.
PN	
XX	20-DEC-2001.
PD	
XX	
PF	14-JUN-2001; 2001WO-US019444.
XX	
PR	15-JUN-2000; 2000US-0212073P.
PR	23-JUN-2000; 2000US-021367P.
PR	30-JUN-2000; 2000US-0215651P.
PR	07-JUL-2000; 2000US-021605P.
PR	13-JUL-2000; 2000US-0218372P.
PR	25-AUG-2000; 2000US-0228056P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Yue H, Lal P, Bandman O, Borowczyk ML, Au-Young J, Lu Y;
PI	Gadgil AR, Tribouley CM, Walla NK, Yao MG, Lu DM, Greenwald SR;
PI	Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YF;
PI	Baughn KR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI	Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI	Grether M, Elliott VS, Thangavelu K, Patra S, Ison CH;
XX	
XX	WPI; 2002-090207/12.
XX	N-PSDB; AAD26473.
XX	

New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development. Cardiovascular and lipid and disease, such as

PT New polypeptides, useful for diagnosing, treating or preventing disorders  
PT of growth and development, cardiovascular and lipid, and diseases such as  
PT cancer, comprise human kinase polypeptides.  
XX  
PS  
XX Claim 1, Page 174-175; 197pp; English.

The invention relates to human kinase P13N proteins and their corresponding cDNAs. A composition containing P13N agonist is useful for treating a disease or condition associated with decreased expression of P13N and a composition comprising P13N antagonist is useful for treating a disease or condition associated with overexpression of P13N. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, osteoarthritis, osteoporosis, narcolepsy, psoriasis, Reiter's syndrome, rheumatoid arthritis, sarcoidosis, Sjogren's syndrome, ulcerative colitis, vitiligo).

CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)  
CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,  
CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio  
CC vascular disease (arteriovenous fistula, hypertension, vasculitis,  
CC vasculitis)

PKIN-26 protein and in gene therapy. The present sequence is human

Seq	Sequence	660 AA;
Query Match	100.0%;	Score 725; DB 5; Length 660;
Best Local Similarity	100.0%;	Pred. No. 5, 5e-74;
Matches 137;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0
QY	1 AVTKERYMQMEETMSSTTLGFRLEGKKKDDGTCNTNFKTKQLAEVTKVLEDFVVDGHHV	60
Db	508 AVTKERYMQMEETMSSTTLGFRLEGKKKDDGTCNTNFKTKQLAEVTKVLEDFVVDGHHV	567
QY	61 LKQKVACLEELREALLETSPFKTHEVVGSSLLFVYDHGIALKVMWIDSGKVALPDDHT	120

NOT 627

**QY**      121 LSHRLPWAEGNREDGYL 137  
         |||||  
**Nb**      62A TSHRTPWAEGNREDGYL 644  
         |||||

RESULT 5  
ABU65211  
ID ABU65211 standard; protein; 683 AA.  
XX  
AC ABU65211;  
XX  
XX 20-MAY-2003 (first entry)  
DT  
XX  
DE Human NOV123a protein.  
XX  
XX NOXV; cytosolic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;  
KM hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;  
XX human.  
XX  
OS Homo sapiens.  
PN WO200272757-A2.  
PD 19-SEP-2002.  
PF 08-MAR-2002; 2002MO-US0606908.  
XX  
XX 08-MAR-2001; 2001US-0274101P.  
PR 08-MAR-2001; 2001US-0274194P.  
PR 08-MAR-2001; 2001US-0274281P.  
PR 08-MAR-2001; 2001US-0274322P.  
PR 09-MAR-2001; 2001US-0274849P.  
PR 12-MAR-2001; 2001US-0275235P.  
PR 13-MAR-2001; 2001US-0275578P.  
PR 13-MAR-2001; 2001US-0275579P.  
PR 13-MAR-2001; 2001US-0275601P.  
PR 14-MAR-2001; 2001US-0276000P.  
PR 15-MAR-2001; 2001US-0276776P.  
PR 19-MAR-2001; 2001US-0276999P.  
PR 20-MAR-2001; 2001US-0277233P.  
PR 20-MAR-2001; 2001US-0277321P.  
PR 21-MAR-2001; 2001US-0277791P.  
PR 21-MAR-2001; 2001US-0277833P.  
PR 22-MAR-2001; 2001US-0278153P.  
PR 26-MAR-2001; 2001US-0278894P.  
PR 27-MAR-2001; 2001US-0278999P.  
PR 27-MAR-2001; 2001US-0279036P.  
PR 28-MAR-2001; 2001US-0279344P.  
PR 30-MAR-2001; 2001US-0279388P.  
PR 30-MAR-2001; 2001US-0279995P.  
PR 30-MAR-2001; 2001US-0280233P.  
PR 02-APR-2001; 2001US-0280802P.  
PR 02-APR-2001; 2001US-0280822P.  
PR 02-APR-2001; 2001US-0280900P.  
PR 04-APR-2001; 2001US-0281194P.  
PR 13-APR-2001; 2001US-0283675P.  
PR 30-APR-2001; 2001US-0287424P.  
PR 02-MAY-2001; 2001US-0288066P.  
PR 03-MAY-2001; 2001US-0288342P.  
PR 03-MAY-2001; 2001US-0288528P.  
PR 15-MAY-2001; 2001US-0291190P.  
PR 16-MAY-2001; 2001US-0291099P.  
PR 16-MAY-2001; 2001US-0291240P.  
PR 30-MAY-2001; 2001US-0294485P.  
PR 31-MAY-2001; 2001US-0294899P.  
PR 31-MAY-2001; 2001US-0294899P.  
PR 18-JUN-2001; 2001US-0299027P.  
PR 19-JUN-2001; 2001US-0299303P.  
PR 19-JUN-2001; 2001US-0299310P.  
PR 10-JUL-2001; 2001US-0304354P.  
PR 31-JUL-2001; 2001US-0309198P.  
PR 16-AUG-2001; 2001US-0312903P.  
PR 10-SEP-2001; 2001US-0318462P.  
PR 12-SEP-2001; 2001US-0318770P.  
PR 27-SEP-2001; 2001US-0325430P.

PR 27-SEP-2001; 2001US-0325681P.  
PR 18-OCT-2001; 2001US-0330380P.  
PR 31-OCT-2001; 2001US-0335301P.  
PR 14-NOV-2001; 2001US-0332172P.  
PR 14-NOV-2001; 2001US-0332271P.  
PR 14-NOV-2001; 2001US-0332712P.  
PR 14-NOV-2001; 2001US-0333184P.  
PR 14-NOV-2001; 2001US-0333722P.  
PR 21-NOV-2001; 2001US-0332094P.  
PR 03-DEC-2001; 2001US-0337426P.  
PR 03-DEC-2001; 2001US-0338092P.  
PR 04-DEC-2001; 2001US-0337185P.  
PR 03-JAN-2002; 2002US-0345705P.  
PR 07-MAR-2002; 2002US-00092900.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Padigar M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L,  
PI Zehrhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;  
PI Patturajan M, Gangoli E, Vernet CM, Guo X, Tchernev V;  
PI Fernandes ER, Caeman SJ, Malyanar UM, Gerlach V, Liu Y, Anderson D;  
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsdbrook JP;  
PI Lepley DW, Rieger DK;  
XX  
XX WPI; 2002-723332/78.  
DR N-PSDB; ABX971178.  
XX  
XX NOXV polypeptides and polynucleotides, useful for preventing or treating  
PT a disorder associated with aberrant NOXV expression or activity e.g.,  
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial  
PT asthma.  
XX  
XX Claim 1; Page 461; 1103pp; English.  
PS  
XX  
XX This invention describes novel human NOXV polypeptides which have  
CC cytosolic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive  
CC activity. Pharmaceutical compositions comprising the NOXV proteins or  
CC nucleic acid molecules or NOXV antibodies are useful for preventing or  
CC treating a disorder associated with aberrant NOXV expression or activity  
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial  
CC asthma. The products of the invention can be used for gene therapy or in  
CC a vaccine. ABU65041-ABU65218 represent the NOXV polypeptides encoded by  
CC ABX97008-ABX97185  
XX  
XX Sequence 683 AA;  
SQ  
Query Match 100.0%; Score 725; DB 5; Length 683;  
Best Local Similarity 100.0%; Pred. No. 5; 8e-74;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVTKPRYQWQREMTSSSTTGFRTGRTGKADGTCNTNPKKTOALEQVTKVLEDFVDDGHV 60  
DB 531 AVTKPRYQWQREMTSSSTTGFRTGRTGKADGTCNTNPKKTOALEQVTKVLEDFVDDGHV 590  
QY 61 ILQKTVACLEBRLREALEISPPFKTHEVVGSSILFEVHDHTGLAKYMTIDFGKTVALLPDHQT 120  
DB 551 ILQKTVACLEBRLREALEISPPFKTHEVVGSSILFEVHDHTGLAKYMTIDFGKTVALLPDHQT 650  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 651 LSHRLPMAEGNREDGYL 667  
RESULT 6  
ADN62073  
ID ADN62073 standard; protein; 683 AA.  
XX  
XX ADN62073;  
AC  
XX  
XX 01-JUL-2004 (first entry)  
DT  
XX  
DE Human novel protein NOV123a.  
XX

KM Human; NOVX; diabetes; obesity; infectious disease; anorexia;  
 cancer-associated cachexia; cancer; neurodegenerative disorder;  
 KM Alzheimer's disease; Parkinson's disease; immune disorder;  
 KM haematopoietic disorder; dyslipidaemia; chronic disease.  
 OS Homo sapiens.  
 PN US2004043382-A1.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 07-MAR-2002; 2002US-00092900.  
 XX  
 PR 08-MAR-2001; 2001US-0274191P.  
 PR 08-MAR-2001; 2001US-0274194P.  
 PR 08-MAR-2001; 2001US-0274281P.  
 PR 08-MAR-2001; 2001US-0274322P.  
 PR 09-MAR-2001; 2001US-0274849P.  
 PR 12-MAR-2001; 2001US-0275235P.  
 PR 13-MAR-2001; 2001US-0275578P.  
 PR 13-MAR-2001; 2001US-0275579P.  
 PR 13-MAR-2001; 2001US-0275601P.  
 PR 14-MAR-2001; 2001US-0276000P.  
 PR 16-MAR-2001; 2001US-0276776P.  
 PR 19-MAR-2001; 2001US-0276994P.  
 PR 20-MAR-2001; 2001US-0277239P.  
 PR 20-MAR-2001; 2001US-0277321P.  
 PR 20-MAR-2001; 2001US-0277327P.  
 PR 20-MAR-2001; 2001US-0277338P.  
 PR 21-MAR-2001; 2001US-0277791P.  
 PR 22-MAR-2001; 2001US-0277833P.  
 PR 23-MAR-2001; 2001US-0278152P.  
 PR 26-MAR-2001; 2001US-0278894P.  
 PR 27-MAR-2001; 2001US-0278999P.  
 PR 27-MAR-2001; 2001US-0279036P.  
 PR 28-MAR-2001; 2001US-0279344P.  
 PR 30-MAR-2001; 2001US-0279995P.  
 PR 30-MAR-2001; 2001US-0280233P.  
 PR 02-APR-2001; 2001US-0280802P.  
 PR 02-APR-2001; 2001US-0280822P.  
 PR 02-APR-2001; 2001US-0280900P.  
 PR 04-APR-2001; 2001US-0281444P.  
 PR 13-APR-2001; 2001US-0283675P.  
 PR 30-APR-2001; 2001US-0287424P.  
 PR 02-MAY-2001; 2001US-0288066P.  
 PR 03-MAY-2001; 2001US-0288342P.  
 PR 03-MAY-2001; 2001US-0288528P.  
 PR 15-MAY-2001; 2001US-0291190P.  
 PR 16-MAY-2001; 2001US-0291099P.  
 PR 16-MAY-2001; 2001US-0291240P.  
 PR 30-MAY-2001; 2001US-0294485P.  
 PR 31-MAY-2001; 2001US-0294889P.  
 PR 31-MAY-2001; 2001US-0294899P.  
 PR 18-JUN-2001; 2001US-0299027P.  
 PR 19-JUN-2001; 2001US-0299303P.  
 PR 19-JUN-2001; 2001US-0299310P.  
 PR 10-JUL-2001; 2001US-0304354P.  
 PR 31-JUL-2001; 2001US-0309198P.  
 PR 16-AUG-2001; 2001US-0312903P.  
 PR 10-SEP-2001; 2001US-0318462P.  
 PR 12-SEP-2001; 2001US-0318770P.  
 PR 27-SEP-2001; 2001US-0325430P.  
 PR 27-SEP-2001; 2001US-0325681P.  
 PR 18-OCT-2001; 2001US-0330388P.  
 PR 31-OCT-2001; 2001US-0335301P.  
 PR 14-NOV-2001; 2001US-0332172P.  
 PR 14-NOV-2001; 2001US-0332271P.  
 PR 14-NOV-2001; 2001US-0332272P.  
 PR 14-NOV-2001; 2001US-0333184P.  
 PR 21-NOV-2001; 2001US-0333272P.  
 PR 03-DEC-2001; 2001US-0332094P.  
 PR 03-DEC-2001; 2001US-0337426P.  
 PR 03-DEC-2001; 2001US-0338092P.

PR 04-DEC-2001; 2001US-0337185P.  
 PR 03-JAN-2002; 2002US-0345705P.  
 XX  
 PA (PADI/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 PA (SHEN/) SHENOY S G.  
 PA (TAUP/) TAUPIER R J.  
 PA (PENA/) PENA C E A.  
 PA (LITL/) LI L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (GUSE/) GUSEV V Y.  
 PA (JIMW/) JI W.  
 PA (GORM/) GORMAN L.  
 PA (MILL/) MILLER C E.  
 PA (KEKU/) KETKUDA R.  
 PA (PATU/) PATTURAJAN M.  
 PA (GANG/) GANGOLLI E A.  
 PA (VERN/) VERNET C A M.  
 PA (GUOX/) GUO X S.  
 PA (TCHE/) TCHERNEV V T.  
 PA (FERN/) FERNANDES E R.  
 PA (CASW/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (GERL/) GERLACH V.  
 PA (LITV/) LITV Y.  
 PA (ANDE/) ANDERSON D W.  
 PA (SPAD/) SPADERNA S K.  
 PA (CATP/) CATTERTON E.  
 PA (LEIT/) LEITE M W.  
 PA (ZHON/) ZHONG H.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (LEPL/) LEPLLEY D M.  
 PA (RIEG/) RIEGER D K.  
 PA (BURG/) BURGESS C E.  
 XX  
 PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L,  
 PI Zethusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Ketkuda R,  
 PI Patturajan M, Gangolli EA, Vernet CM, Guo XS, Tchernev VT;  
 PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y,  
 PI Spaderna DW, Spaderna SK, Catterton E, Leite MW, Zhong H;  
 PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
 XX  
 DR MPI; 2004-225693/21.  
 DR N-PSDB; ADM62072.  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for diagnosing,  
 PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,  
 PT infection or obesity, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 PS Claim 1; SEQ ID NO 342; 786pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide (designated NOVX, or  
 CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino  
 CC acid sequences (and their mature forms, variants and fragments). Also  
 CC included are an isolated nucleic acid molecule encoding NOVX, a vector  
 CC comprising the nucleic acid, a cell comprising the vector, methods for  
 CC determining the presence or amount of the polypeptide or the nucleic acid  
 CC molecule in a sample, methods for determining the presence of or  
 CC predisposition to a disease associated with altered levels of expression  
 CC of the above polypeptide or nucleic acid molecule in a first mammalian  
 CC subject, a method for identifying an agent that binds to the above  
 CC polypeptide, a method for identifying a potential therapeutic agent for  
 CC use in the treatment of a pathology that is related to aberrant  
 CC expression or physiological interactions of the polypeptide, a method of  
 CC screening for a modulator of activity or of latency or predisposition to  
 CC a pathology associated with the polypeptide and a method for modulating  
 CC the activity of the polypeptide cited above. The composition and methods  
 CC are useful for diagnosing, preventing or treating diseases such as  
 CC diabetes, obesity, infectious diseases, anorexia, cancer-associated  
 CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or  
 CC Parkinson's disease, immune disorders, haematopoietic disorders,  
 CC dyslipidaemias, and other chronic diseases. These may also be used in

CC chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The polypeptides are also useful as vaccines. The  
CC present sequence represents a NOVX protein of the invention.

XX Sequence 683 AA;

Query Match 100.0%; Score 725; DB 8; Length 683;

Best Local Similarity 100.0%; Pred. No. 5.8e-74; Indels 0; Gaps 0;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 AVTKRYMQWRETMSTSTLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDHV 60

CC 531 AVTKRYMQWRETMSTSTLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDHV 590

CC 61 ILQKYVACLEBELRALISPFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHOT 120

CC 591 ILQKYVACLEBELRALISPFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHOT 650

DB 121 LSHRLPWAEGNREDGYL 137

DB 651 LSHRLPWAEGNREDGYL 667

RESULT 7

ID AEB87638 standard; protein; 683 AA.

AC AEB87638;

DT 20-OCT-2005 (first entry)

DE Human inositol-trisphosphate 3-kinase C (ITPKC).

KM inositol-trisphosphate 3-kinase C; ITPKC;

KM insulin-like growth factor receptor modulator; cytosolic; cancer;

KM neoplasm; gene therapy; antisense therapy; antibody therapy;

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 393..678 /note="inositol polyphosphate kinase domain"

XX WO2005072475-A2.

XX 11-AUG-2005.

XX 27-JAN-2005; 2005WO-US003560.

XX 28-JAN-2004; 2004US-0539837P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Francis-Iang H, Parks AL, Shaw KJ, Bjerke LM;

XX Heuer TS;

XX WPI; 2005-555620/56.

XX N-PSDB; AEB87639.

XX REFSEQ; NP\_079470.

XX Identifying candidate Insulin Growth Factor Receptor pathway modulating

XX agents useful for diagnosing or treating, for e.g. cancer, comprises

XX triphosphate 3-kinase.

XX Dieckmeyer, SEQ ID NO 10; 87pp; English.

XX The present sequence is the protein sequence of human inositol-

XX triphosphate 3-kinase C (ITPKC). A dominant loss of function screening

XX was carried out in Drosophila to identify genes that interact with or

XX modulate the insulin-like growth factor receptor (IGFR) signaling

XX pathway. Modifiers of the IGFR pathway were isolated, and the human

CC orthologs of these modifiers were identified as ITPKs. The invention

CC provides methods for using these IGFR modifier genes and polypeptides to

CC identify ITPK-modulating agents that are candidate therapeutic agents for

CC use in the treatment of disorders associated with defective or impaired

CC IGF function and/or ITPK function. In one embodiment, candidate ITPK

CC modulator agents are tested in an assay system comprising an ITPK

CC polypeptide or nucleic acid. Agents that produce a change in the activity

CC of the assay system relative to controls are identified as candidate IGFR

CC modulating agents. The screening assay system may be a binding assay, an

CC apoptosis assay, a cell proliferation assay, an angiogenesis assay or a

CC hypoxia induction assay. Preferred ITPK-modulating agents include small

CC molecule modulators, nucleic acid molecules such as antisense oligomers

CC or phosphorothioate morpholino oligomers, and antibodies. A probe for

CC ITPK expression is used in a claimed method for diagnosing a disease,

CC particularly cancer.

CC Sequence 683 AA;

CC Query Match 100.0%; Score 725; DB 9; Length 683;

CC Best Local Similarity 100.0%; Pred. No. 5.8e-74; Indels 0; Gaps 0;

CC Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 AVTKRYMQWRETMSTSTLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDHV 60

CC 531 AVTKRYMQWRETMSTSTLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDHV 590

CC 61 ILQKYVACLEBELRALISPFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHOT 120

CC 591 ILQKYVACLEBELRALISPFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHOT 650

DB 121 LSHRLPWAEGNREDGYL 137

DB 651 LSHRLPWAEGNREDGYL 667

RESULT 8

ID AAM41393 standard; protein; 687 AA.

AC AAM41393;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6324.

KM Human; noctropic; immunosuppressant; cytosolic; gene therapy; cancer;

KM peripheral nervous system; neuropathy; central nervous system; CNS;

KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KM chemokine; thrombolytic; drug screening; arthritis; inflammation;

XX leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00588042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YR, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR MPI: 2001-442253/47.  
XX N-PSDB; AA160549.  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 2; SEQ ID NO 6324; 10078bp; English.  
XX  
CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AA38642-AA42213) with neurotropic,  
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 687 AA;  
  
Query Match 100.0%; Score 725; DB 4; Length 687;  
Best Local Similarity 100.0%; Pred. No. 5.8e-74;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AATKRRYQWRRTMSSTSLGFRIRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDH 60  
DB 535 AATKRRYQWRRTMSSTSLGFRIRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDH 594  
61 ILQKTVACLEBEIRALEISPPFKTHEVVGSSLLFVHDHTGLAKWMIIDFGKTVALLPDHOT 120  
DB 595 ILQKTVACLEBEIRALEISPPFKTHEVVGSSLLFVHDHTGLAKWMIIDFGKTVALLPDHOT 654  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 655 LSHRLPMAEGNREDGYL 671  
DB  
  
RESULT 9  
AAM39607  
ID AAM39607 standard; protein; 711 AA.  
XX  
AC AAM39607;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2752.  
XX  
XX Human; neurotropic; immunosuppressant; cytoskeletal; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
XX leukaemia.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
XX PD 26-JUL-2001.  
XX  
XX PF 26-DEC-2000; 2000MO-US034263.  
XX  
XX PR 23-DEC-1999; 99US-00471275.  
XX  
XX PR 21-JAN-2000; 2000US-00488725.  
XX

PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HSEB-) HSEB INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;  
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
XX Zhou P, Goodrich R, Drmanac RT;  
XX  
DR MPI: 2001-442253/47.  
XX N-PSDB; AA158763.  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 4; SEQ ID NO 2752; 10078bp; English.  
XX  
CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AA38642-AA42213) with neurotropic,  
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 711 AA;  
  
Query Match 100.0%; Score 725; DB 4; Length 711;  
Best Local Similarity 100.0%; Pred. No. 6.1e-74;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AATKRRYQWRRTMSSTSLGFRIRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDH 60  
DB 559 AATKRRYQWRRTMSSTSLGFRIRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDH 618  
61 ILQKTVACLEBEIRALEISPPFKTHEVVGSSLLFVHDHTGLAKWMIIDFGKTVALLPDHOT 120  
DB 619 ILQKTVACLEBEIRALEISPPFKTHEVVGSSLLFVHDHTGLAKWMIIDFGKTVALLPDHOT 678  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 679 LSHRLPMAEGNREDGYL 695  
DB  
  
RESULT 10  
ABB09772  
ID ABB09772 standard; protein; 461 AA.  
XX  
AC ABB09772;  
XX  
DT 22-JUL-2002 (first entry)  
XX  
XX Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-A.  
XX  
XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
XX endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
XX chronic infection; arthritis; cancer; cystic fibrosis;  
XX Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
XX DIP3K1, DIP3K2.  
XX



OS Homo sapiens.  
XX  
PN FR2813612-A1.  
XX  
PD 08-MAR-2002.  
XX  
PF 07-SEP-2000; 2000FR-00011397.  
XX  
PR 07-SEP-2000; 2000FR-00011397.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
PI Tricoire H, Monnier V, Pret AM, Cabet DE, Brissard J, Vandurka P,  
PI Glatardot F;  
XX  
DR WPI: 2002-260343/31.  
XX  
DR N-PSDB: ABL56444.  
XX  
PT New proteins with inositol-triphosphate kinase activity, useful e.g. for  
PT treating oxidative stress and neurodegeneration.  
XX  
XX  
PS Claim 4; Fig 3; 69pp; French.  
XX  
CC The present sequence represents inositol-1,4,5-triphosphate 3 (IP3)  
CC kinase-A protein. The specification also describes Drosophila IP3 kinase  
CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
CC 1,4,5-triphosphate) kinase activity. The specification describes the use  
CC of IP3 kinase proteins to prepare compositions for treating diseases  
CC associated with oxidative stress, stress of the endoplasmic reticulum or  
CC neurodegeneration, particularly of the retina. Overexpression of IP3  
CC kinase protects cells against the damaging effects of free radicals  
CC without altering free radical homeostasis within the cell. The IP3  
CC proteins are used for treating disorders associated with oxidative  
CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
CC particularly chronic infection (such as arthritis and some forms of  
CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases; and  
CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
CC kinase proteins are used to identify phenotypic alterations associated  
CC with loss of this gene  
XX  
SQ Sequence 461 AA;  
XX  
Query Match 69.5%; Score 504; DB 5; Length 461;  
Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;  
OY 1 AVTKPRYWMQREMTSSTLTGFRIGIKKADGTCNTNFKTQALQVYTKVLEDPVGDHV 60  
DB 309 AVTKPRYWMQREMTSSTLTGFRIGIKKADGSCSTDFKTRSRQVLRVEEFGDDE 368  
OY 61 ILQKYVACLEELREALIEISPFKTHEVVGSSLLFVHDHTGLAKVWMDFGKTVALLPDHQT 120  
DB 369 VLRRYVLRNLOQIRDTLSESEFFRRHVEVGSLLFPHDCHAGVWLIDFGKTVLPDQI 428  
OY 121 LSHRLPMAEGNREDGYL 137  
DB 429 LDHRRPMEEGNREDGYL 445  
XX  
RESULT 11  
ADO44008  
ID ADO44008 standard; protein; 461 AA.  
XX  
AC ADO44008;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Amino acid sequence of human ID-MYO-inositol triphosphate 3 kinase A.  
XX  
XX protein complex; neurological disease; stroke; neurodegeneration;  
KW Wallerian degeneration; Alzheimer's disease; neurological disorder;  
KW epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;  
KW atherosclerosis; ID-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2;

KW ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha;  
KW Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP;  
KW FLJ14653 NT2RP2002252; FLJ30839 PEBRA2002429; HERC2;  
KW inositol polyphosphate-5-phosphatase; inositol-1; 4;  
KW 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;  
KW Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;  
KW Pushover; S-adenosylhomocysteinease;  
KW secretory carrier-associated membrane protein 2; surfactant protein 2;  
KW ubiquitin carboxyl terminal hydrolase 11;  
KW upstream regulatory element binding protein 1; Vartul;  
KW Werner's syndrome helicase interacting protein; WHIP;  
KW X-ray repair cross complementing protein 4.  
XX  
OS Homo sapiens.  
XX  
PN WO2004031242-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 11-SEP-2003; 2003WO-EP010110.  
XX  
PR 12-SEP-2002; 2002EP-00020495.  
PR 12-SEP-2002; 2002EP-00020496.  
PR 12-SEP-2002; 2002EP-00020497.  
XX  
PA (CELL-) CELLZOME AG.  
XX  
PI Bouwmeester T, Drewes G, Jackson D, Heltenbein G, Schirle M;  
PI Kuester B, Hopf C;  
XX  
DR WPI: 2004-316467/29.  
XX  
PT New complex comprising at least one first protein, and at least one  
PT second protein, useful for treating stroke, Alzheimer's disease,  
PT neurological disorders such as epilepsy, and inflammatory conditions such  
PT as ulcerative colitis.  
XX  
XX  
PS Example; Page 243-245; 287pp; English.  
XX  
CC The specification describes protein complexes involved in cellular  
CC processes which have been shown to be critical for the development of  
CC various forms of neurological diseases. Three protein complexes were  
CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3  
CC protein complex. The protein complex are useful for treating diseases and  
CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,  
CC Alzheimer's disease, neurodegeneration such as epilepsy, and  
CC inflammatory conditions such as ulcerative colitis, Crohn's disease or  
CC atherosclerosis. Proteins identified as being part of the protein  
CC complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,  
CC ASK1, ASK2, ASK3, CAMKII beta, CAMKII delta, CAMKII gamma, casein kinase  
CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,  
CC FLJ14653 NT2RP2002252, FLJ30839 PEBRA2002429, HERC2, two hypothetical  
CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,  
CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441,  
CC MSTP030, Nek9, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1  
CC precursor, Pushover, a putative S-adenosylhomocysteinease, secretory  
CC carrier-associated membrane protein 2, surfactant protein 2, ubiquitin  
CC carboxyl terminal hydrolase 11, upstream regulatory element binding  
CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),  
CC X-ray repair cross complementing protein 4 (isoform 1). The present  
CC sequence represents ID-MYO-inositol triphosphate 3 kinase A.  
XX  
SQ Sequence 461 AA;  
XX  
Query Match 69.5%; Score 504; DB 8; Length 461;  
Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;  
OY 1 AVTKPRYWMQREMTSSTLTGFRIGIKKADGTCNTNFKTQALQVYTKVLEDPVGDHV 60  
DB 309 AVTKPRYWMQREMTSSTLTGFRIGIKKADGSCSTDFKTRSRQVLRVEEFGDDE 368  
OY 61 ILQKYVACLEELREALIEISPFKTHEVVGSSLLFVHDHTGLAKVWMDFGKTVALLPDHQT 120



DB 369 VLRRYLNRLQGIKRDLEVESEFFRRHREYVIGSSLLFVHDHCHRAAGWVLIDFGKTTPLPDQGI 428  
 QY 121 LSHRLPMAEGNREDEYL 137  
 DB 429 LDHRRPMEEGNREDEYL 445

RESULT 12  
 AEB87636  
 ID AEB87636 standard; protein; 461 AA.  
 XX AEB87636;  
 AC AEB87636;  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 DE Human inositol-trisphosphate 3-kinase A (ITPKA).  
 XX  
 KW Inositol-trisphosphate 3-kinase A; ITPKA;  
 KW inulin-like growth factor receptor modulator; cytosolic; cancer;  
 KW neoplasm; gene therapy; antisense therapy; antibody therapy;  
 KW drug screening; diagnosis; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FH 171..456  
 FT Domain /note="Inositol polyphosphate kinase domain"  
 FT  
 XX  
 PN WO2005072475-A2.  
 XX  
 PD 11-AUG-2005.  
 XX  
 PF 27-JAN-2005; 2005WO-US003560.  
 XX  
 PR 28-JAN-2004; 2004US-0539837P.  
 XX  
 PA (EXEL-) EXELIXIS INC.  
 XX  
 PI Friedman L, Francis-Lang H, Parks AL, Shaw KJ, Bjerke LM,  
 PI Heuer TS;  
 XX  
 DR WPI; 2005-555620/56.  
 DR N-PSDB; AEB87629, AEB87630.  
 DR  
 XX RESEQ; NP\_002211.  
 DR  
 PT Identifying candidate Insulin Growth Factor Receptor pathway modulating  
 PT agents useful for diagnosing or treating, for e.g. cancer, comprises  
 PT screening for agents that modulate the activity of Inositol 1,4,5-  
 PT triphosphate 3-kinase.  
 XX  
 PS Disclosure; SEQ ID NO 8; 87bp; English.  
 XX  
 CC The present sequence is the protein sequence of human inositol-  
 CC trisphosphate 3-kinase A (ITPKA). A dominant loss of function screening  
 CC was carried out in *Drosophila* to identify genes that interact with or  
 CC modulate the inulin-like growth factor receptor (IGFR) signaling  
 CC pathway. Modifiers of the IGFR pathway were isolated, and the human  
 CC orthologs of these modifiers were identified as ITPKs. The invention  
 CC provides methods for using these IGFR modifier genes and polypeptides to  
 CC identify ITPK-modulating agents that are candidate therapeutic agents for  
 CC use in the treatment of disorders associated with defective or impaired  
 CC IGFR function and/or ITPK function. In one embodiment, candidate ITPK  
 CC modulator agents are tested in an assay system comprising an ITPK  
 CC polypeptide or nucleic acid. Agents that produce a change in the activity  
 CC of the assay system relative to controls are identified as candidate IGFR  
 CC modulating agents. The screening assay system may be a binding assay, an  
 CC apoptosis assay, a cell proliferation assay, an angiogenesis assay or a  
 CC hypoxic induction assay. Preferred ITPK-modulating agents include small  
 CC molecule modulators, nucleic acid molecules such as antisense oligomers  
 CC or phosphorocholate morpholino oligomers, and antibodies. A probe for  
 CC ITPK expression is used in a claimed method for diagnosing a disease,  
 CC particularly cancer.

XX  
 SQ Sequence 461 AA;  
 Query Match 69.5%; Score 504; DB 9; Length 461;  
 Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 AVTKRYNQWRMTSSTSLGRIEIGIKKADGTQNTNFKTQALKEQVTKLEDPVGDHV 60  
 DB 309 AVTKPRYMQWRBGSSSTSLGRIEIGIKKAGSCSTDPKTRSRQVLRVEEFVQSDDE 368  
 QY 61 ILQKTVACLEELREALISPFKTEHVVGSLLFVHDHCHRAAGWVLIDFGKTTVALPDQQT 120  
 DB 369 VLRRYLNRLQGIKRDLEVESEFFRRHREYVIGSSLLFVHDHCHRAAGWVLIDFGKTTPLPDQGI 428  
 QY 121 LSHRLPMAEGNREDEYL 137  
 DB 429 LDHRRPMEEGNREDEYL 445

RESULT 13  
 ABB09782  
 ID ABB09782 standard; protein; 477 AA.  
 XX  
 AC ABB09782;  
 XX  
 DT 22-JUL-2002 (first entry)  
 XX  
 DE Amino acid sequence of human inositol-1,4,5-trisphosphate 3 kinase-A.  
 XX  
 KW IP3 kinase; inositol-1,4,5-trisphosphate kinase; enzyme; oxidative stress;  
 KW endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
 KW chronic infection; arthritis; cancer; cystic fibrosis;  
 KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KW DIP3K1; DIP3K2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220742-A1.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 31-AUG-2001; 2001WO-FR002708.  
 XX  
 PR 07-SEP-2000; 2000FR-00011397.  
 XX  
 PA (CNRS ) CENT NAT RECH SCI.  
 XX  
 PI Tricolre H, Monnier V, Pret A, Busson DE, Zahraoui J, Vandurka P;  
 PI Girardot F;  
 XX  
 DR WPI; 2002-260343/31.  
 DR  
 XX  
 PT New proteins with inositol-trisphosphate kinase activity, useful e.g. for  
 PT treating oxidative stress and neurodegeneration.  
 XX  
 PS Claim 4; Page 53-54; 64bp; French.  
 XX  
 CC The present sequence represents inositol-1,4,5-trisphosphate 3 (IP3)  
 CC kinase-A protein. The specification also describes *Drosophila* IP3 kinase  
 CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
 CC 1,4,5-trisphosphate) kinase activity. The specification describes the use  
 CC of IP3 kinase proteins to prepare compositions for treating diseases  
 CC associated with oxidative stress, stress of the endoplasmic reticulum or  
 CC neurodegeneration, particularly of the retina. Overexpression of IP3  
 CC kinase protects cells against the damaging effects of free radicals  
 CC without altering free radical homeostasis within the cell. The IP3  
 CC proteins are used for treating disorders associated with oxidative  
 CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
 CC particularly chronic infection (such as arthritis and some forms of  
 CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and  
 CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated

CC with loss of this gene. This specification is equivalent to FR2813612  
 XX  
 SQ Sequence 477 AA;

Query Match 69.5%; Score 504; DB 5; Length 477;  
 Best Local Similarity 66.4%; Pred. No. 9.9e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 AVTKPRMQRMTSSSTSTGFRLEGKKADGTCNTNFKKTQALQVTKYLEDFVGDH 60  
 DB 309 AVTKPRMQRMTSSSTSTGFRLEGKKADGTCNTNFKKTQALQVTKYLEDFVGDH 368  
 QY 61 ILQKYVACBELREALISPFKTHEVVGSSLLFVHDHTGLAKYMWIDFGKTVLPDHT 120  
 DB 369 VLRRYLRLQIQIRLTLEVSEPFRRHEVIGSSLLFVHDHCHRAQVWLIDFGKTVLPDHT 428  
 QY 121 LSHRLPWAEGNREDGYL 137  
 DB 429 LDHRRPWEQGNREDGYL 445

RESULT 14  
 ABB09773

ID ABB09773 standard; protein; 472 AA.

AC ABB09773;

DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-B.

XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
 KM endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
 KM chronic infection; arthritis; cancer; cystic fibrosis; retinopathy;  
 KM Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KM DIP3K1; DIP3K2.

XX Homo sapiens.

OS

XX FR2813612-A1.

PN 08-MAR-2002.

PD 07-SEP-2000; 2000FR-00011397.

PF 07-SEP-2000; 2000FR-00011397.

PR (CNRS ) CNRS CENT NAT RECH SCT.

PA Tricoire H, Monnier V, Pret AM, Cabet DE, Briesard J, Vandurka P;

PI Girardot F;

XX WPI, 2002-260343/31.

DR N-PSDB; ABL56445.

XX New proteins with inositol-triphosphate kinase activity, useful e.g. for

PT treating oxidative stress and neurodegeneration.

PS Claim 4; Fig 4; 69pp; French.

XX The present sequence represents inositol-1,4,5-triphosphate 3 (IP3)  
 CC kinase-B protein. The specification also describes Drosophila IP3 kinase  
 CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
 CC 1,4,5-triphosphate) kinase activity. The specification describes the use  
 CC of IP3 kinase proteins to prepare compositions for treating diseases  
 CC associated with oxidative stress, stress of the endoplasmic reticulum or  
 CC neurodegeneration, particularly of the retina. Overexpression of IP3  
 CC kinase protects cells against the damaging effects of free radicals  
 CC without altering free radical homeostasis within the cell. The IP3  
 CC proteins are used for treating disorders associated with oxidative  
 CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
 CC particularly chronic infection (such as arthritis and some forms of  
 CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and

CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated  
 CC with loss of this gene  
 XX

SQ Sequence 472 AA;

Query Match 68.0%; Score 493; DB 5; Length 472;  
 Best Local Similarity 67.9%; Pred. No. 1.8e-47;  
 Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKPRMQRMTSSSTSTGFRLEGKKADGTCNTNFKKTQALQVTKYLEDFVGDH 60  
 DB 316 AVTKPRMQRMTSSSTSTGFRLEGKKADGTCNTNFKKTQALQVTKYLEDFVGDH 375  
 QY 61 ILQKYVACBELREALISPFKTHEVVGSSLLFVHDHTGLAKYMWIDFGKTVLPDHT 120  
 DB 376 ILIAYRDLKAITTLEVSEPFRRHEVIGSSLLFHDKQALYMWIDFGKTVLPDHT 435  
 QY 121 LSHRLPWAEGNREDGYL 137  
 DB 436 LDHVPWEQGNREDGYL 452

RESULT 15  
 ABB09783

ID ABB09783 standard; protein; 472 AA.

AC ABB09783;

DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-B.

XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
 KM endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
 KM chronic infection; arthritis; cancer; cystic fibrosis;  
 KM Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KM DIP3K1; DIP3K2.

XX Homo sapiens.

OS

XX WO200220742-A1.

PN 14-MAR-2002.

PD 31-AUG-2001; 2001WO-FR002708.

PF 07-SEP-2000; 2000FR-00011397.

PR (CNRS ) CENT NAT RECH SCT.

PA Tricoire H, Monnier V, Pret A, Busson DE, Zahraoui J, Vandurka P;

PI Girardot F;

XX WPI, 2002-260343/31.

DR New proteins with inositol-triphosphate kinase activity, useful e.g. for

PT treating oxidative stress and neurodegeneration.

PS Claim 4; Page 54-56; 64pp; French.

XX The present sequence represents inositol-1,4,5-triphosphate 3 (IP3)  
 CC kinase-B protein. The specification also describes Drosophila IP3 kinase  
 CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
 CC 1,4,5-triphosphate) kinase activity. The specification describes the use  
 CC of IP3 kinase proteins to prepare compositions for treating diseases  
 CC associated with oxidative stress, stress of the endoplasmic reticulum or  
 CC neurodegeneration, particularly of the retina. Overexpression of IP3  
 CC kinase protects cells against the damaging effects of free radicals  
 CC without altering free radical homeostasis within the cell. The IP3  
 CC proteins are used for treating disorders associated with oxidative  
 CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
 CC particularly chronic infection (such as arthritis and some forms of



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GenCore version 5.1.8  
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OM protein - protein search, using SW model

Run on: May 21, 2006, 04:20:44 / Search time 38 Seconds  
(without alignments)  
346.887 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725

Sequence: 1 AVTKPRYQMRETMSTSTL.....HQTLSRLPMAGNREDGYL 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	69.8	459	2	1D-myo-inositol-tr
2	504	69.5	461	2	1D-myo-inositol-tr
3	493	68.0	472	2	1D-myo-inositol-tr
4	493	68.0	946	2	inositol 1,4,5-tri
5	487	67.2	673	2	1D-myo-inositol-tr
6	487	67.2	394	2	1D-myo-inositol-tr
7	487	67.2	321	2	1D-myo-inositol-tr
8	487	67.2	321	2	1D-myo-inositol-tr
9	487	67.2	321	2	1D-myo-inositol-tr
10	487	67.2	321	2	1D-myo-inositol-tr
11	487	67.2	321	2	1D-myo-inositol-tr
12	487	67.2	321	2	1D-myo-inositol-tr
13	487	67.2	321	2	1D-myo-inositol-tr
14	487	67.2	321	2	1D-myo-inositol-tr
15	487	67.2	321	2	1D-myo-inositol-tr
16	487	67.2	321	2	1D-myo-inositol-tr
17	487	67.2	321	2	1D-myo-inositol-tr
18	487	67.2	321	2	1D-myo-inositol-tr
19	487	67.2	321	2	1D-myo-inositol-tr
20	487	67.2	321	2	1D-myo-inositol-tr
21	487	67.2	321	2	1D-myo-inositol-tr
22	487	67.2	321	2	1D-myo-inositol-tr
23	487	67.2	321	2	1D-myo-inositol-tr
24	487	67.2	321	2	1D-myo-inositol-tr
25	487	67.2	321	2	1D-myo-inositol-tr
26	487	67.2	321	2	1D-myo-inositol-tr
27	487	67.2	321	2	1D-myo-inositol-tr
28	487	67.2	321	2	1D-myo-inositol-tr
29	487	67.2	321	2	1D-myo-inositol-tr

30	71.5	9.9	715	2	B75135	DNA helicase relat
31	71.5	9.9	807	2	E90523	leucyl-trna synth
32	71	9.8	205	2	AB1903	hypothetical prote
33	71	9.8	427	2	S5776	cysteine proteinas
34	71	9.8	430	2	QJ0120	hypothetical prote
35	71	9.8	1446	2	TJ0916	carboxypeptidase D
36	71	9.8	2137	1	SUHUB	spectrin beta chai
37	70.5	9.7	366	1	A46704	aryl-alcohol dehyd
38	70.5	9.7	497	2	E96774	probable cytochrom
39	70.5	9.7	640	1	VCNRPV	env polypeptid pr
40	70.5	9.7	676	1	VCNRPV	env polypeptid pr
41	70.5	9.7	967	2	T41672	probable b-zip tra
42	70.5	9.7	2030	2	T33162	hypothetical prote
43	70	9.7	286	2	H66664	outer membrane lip
44	70	9.7	617	2	S37744	endo-exonuclease y
45	70	9.7	644	2	S15464	gp70 protein - mur

## ALIGNMENTS

```
RESULT 1
S13064
1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) A - rat
N:Alternate names: inositol-1,4,5-trisphosphate 3-kinase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S13064; A34854; S56747
R:Takazawa, K.; Vandekerckhove, J.; Dumont, J.E.; Erneux, C.
Biochem. J. 272, 107-112, 1990
A>Title: Cloning and expression in Escherichia coli of a rat brain cDNA encoding a Ca(2+)
A:Reference number: S13064; MUID:91090700; PMID:2176078
A:Accession: S13064
A:Molecule type: mRNA
A:Residues: 1-459 <TR>
A:Cross-references: UNIPROT:P17105; UNIPARC:UPI000012D7C2; GB:X56917; NID:G56388; PIDN:C
R:Choi, K.Y.; Kim, H.K.; Lee, S.Y.; Moon, K.H.; Sim, S.S.; Kim, J.W.; Chung, H.K.; Rhee,
Science 248, 64-66, 1990
A>Title: Molecular cloning and expression of a complementary DNA for inositol 1,4,5-tris
A:Reference number: A34854; MUID:90208336; PMID:2157285
A:Accession: A34854
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 10-459 <CHO>
A:Cross-references: UNIPARC:UPI00001679B7; GB:M29787; NID:G204987; PIDN:AAA1457.1; PID:
R:Communi, D.; Lecocq, R.; Vanweyenbergh, V.; Erneux, C.
Biochem. J. 310, 109-115, 1995
A>Title: Active site labelling of inositol 1,4,5-trisphosphate 3-kinase A by phenylglyox
A:Reference number: S56747; MUID:95374430; PMID:7646431
A:Accession: S56747
A:Molecule type: protein
A:Residues: 315-326 <COM>
A:Cross-references: UNIPARC:UPI0000179A9C
A:Experimental source: brain
C:Function:
A:Description: catalyzes the phosphorylation of inositol-1,4,5-trisphosphate to inositol-
A:Keywords: brain; phosphoprotein; phosphotransferase
F:119/Binding site: phosphate (Ser) (covalent) (by cAMP- and calmodulin-dependent kinase
F:119/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:130/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #statu
F:136/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
Query Match 69.8%; Score 506; DB 2; Length 459;
Best Local Similarity 67.2%; Pred. No. 3.3e-40;
Matches 92; Conservative 22; Mismatches 23; Indels 0; Gaps 0;
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Db 367 VLKRYLNRLOQIRDTLEISDFRRHEVIGSSLLFVHDCRAGVWLIDFGKTPPLPDQOI 426  
QY 121 LSHRLPWAEGNRDEGYL 137  
Db 427 LDHRRPWEENRDEGYL 443

## RESULT 2

JN0129  
ID-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) A - human  
N/Alternate names: inositol-1,4,5-trisphosphate 3-kinase A  
C/Species: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C/Accession: JN0129; S13559  
R/Takazawa, K.; Perret, J.; Dumont, J.E.; Erneux, C.  
Biochem. Biophys. Res. Commun. 174, 529-535, 1991  
A/Title: Molecular cloning and expression of a human brain inositol 1,4,5-trisphosphate  
A/Reference number: JN0129; MUID:91128380; PMID:1847047  
A/Accession: JN0129  
A/Molecule type: mRNA  
A/Residues: 1-461 <TKL1>  
A/Cross-references: UNIPROT:P23677; UNIPARC:UPI000049A1A; EMBL:X54938; NID:932104; PID:  
R/Takazawa, K.; Perret, J.; Dumont, J.E.; Erneux, C.  
Nucleic Acids Res. 18, 7141, 1990  
A/Title: Human brain inositol 1,4,5-trisphosphate 3-kinase cDNA sequence.  
A/Reference number: S13559; MUID:91088302; PMID:2175886  
A/Accession: S13559  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-461 <TKX2>  
A/Cross-references: UNIPARC:UPI000049A1A; EMBL:X54938; NID:932104; PID:CA38700.1; PID:  
C/Genetics:  
A/Gene: GDB:ITPKA  
A/Cross-references: GDB:126863; OMIM:147521  
A/Map position: 15q15.1-15q21.1  
C/Function:  
A/Description: catalyzes the phosphorylation of inositol-1,4,5-trisphosphate to inositol-  
A/Keywords: phosphoprotein; phosphorylation  
F/11/Binding site: phosphate (Ser) (covalent) (by CAMP- and calmodulin-dependent kinase  
F/17/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F/31/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #stat  
F/38/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
Query Match 69.5%; Score 504; DB 2; Length 461;  
Best Local Similarity 66.4%; Pred. No. 5.2e-40;  
Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;  
QY 1 AVTKPRYMQWRETNSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
Db 309 AVTKPRYMQWREGSSSTTLGFRIEIGIKKADGSCSTDPKTTRSEQVLRVEEFVQGDDE 368  
QY 61 ILQKYVACLELRALISPPFKTHEVVGSSLLFVHDTGLAKYWMIDFGKTVLPPHOT 120  
Db 369 VLRSYLNRLQOIRLTLEVSFFRRHEVIGSSLLFVHDCRAGVWLIDFGKTPPLPDQOI 428  
QY 121 LSHRLPWAEGNRDEGYL 137  
Db 429 LDHRRPWEENRDEGYL 443

## RESULT 3

S17682  
ID-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human  
N/Alternate names: inositol-1,4,5-trisphosphate 3-kinase B  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
C/Accession: S17682  
R/Takazawa, K.; Perret, J.; Dumont, J.E.; Erneux, C.  
Biochem. J. 278, 883-886, 1991  
A/Title: Molecular cloning and expression of a new putative inositol 1,4,5-trisphosphate  
A/Reference number: S17545; MUID:91378954; PMID:1654894  
A/Accession: S17682

A/Molecule type: mRNA  
A/Residues: 1-472 <TKX>  
A/Cross-references: UNIPARC:UPI000049A1B; EMBL:X57206; NID:933990; PID:CA440491.1; PID:  
C/Genetics:  
A/Gene: GDB:ITPKB  
A/Cross-references: GDB:128973; OMIM:147522  
A/Map position: 1q41-1q43  
C/Keywords: phosphotransferase  
Query Match 68.0%; Score 493; DB 2; Length 472;  
Best Local Similarity 67.9%; Pred. No. 5.9e-39;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;  
QY 1 AVTKPRYMQWRETNSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
Db 316 AVTKPRYMQWRETNSTSTLGFRIEIGIKKEDGTVNRPFKTKTRREQVTEAFREFTKGNHN 375  
QY 61 ILQKYVACLELRALISPPFKTHEVVGSSLLFVHDTGLAKYWMIDFGKTVLPPHOT 120  
Db 376 ILIAYRDLKAIKRTTLEVSFFRCHVEVIGSSLLFIHDKKEQAKYWMIDFGKTPPLPDQOT 435  
QY 121 LSHRLPWAEGNRDEGYL 137  
Db 436 LDHDPVWQEGNRDEGYL 452

## RESULT 4

JC7810  
inositol 1,4,5-trisphosphate 3-kinase B - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 03-Jun-2002  
C/Accession: JC7810  
R/Dewaste, V.; Roymans, D.; Moreau, C.; Erneux, C.  
Biochem. Biophys. Res. Commun. 291, 400-405, 2002  
A/Title: Cloning and expression of a full-length cDNA encoding human inositol 1,4,5-trisph  
A/Reference number: JC7810; PMID:11846419; MUID:21835501  
A/Contents: Frontal cortex  
A/Molecule type: mRNA  
A/Accession: JC7810  
A/Residues: 1-946 <DEM>  
A/Cross-references: UNIPARC:UPI000017CD41; GB:Y18024  
C/Comment: This enzyme, an isoenzyme of inositol 1,4,5-trisphosphate (Ino3p) 3-kinase, ca  
of calcium homeostasis. This enzyme is particularly sensitive to Ca2+ in the presence of

Query Match 68.0%; Score 493; DB 2; Length 946;  
Best Local Similarity 67.9%; Pred. No. 1.3e-38;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;  
QY 1 AVTKPRYMQWRETNSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
Db 790 AVTKPRYMQWRETNSTSTLGFRIEIGIKKEDGTVNRPFKTKTRREQVTEAFREFTKGNHN 849  
QY 61 ILQKYVACLELRALISPPFKTHEVVGSSLLFVHDTGLAKYWMIDFGKTVLPPHOT 120  
Db 850 ILIAYRDLKAIKRTTLEVSPPFKCHEVIGSSLLFIHDKKEQAKYWMIDFGKTPPLPDQOT 909  
QY 121 LSHRLPWAEGNRDEGYL 137  
Db 910 LDHDPVWQEGNRDEGYL 926

## RESULT 5

S41053  
ID-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - rat  
N/Alternate names: IP(3) 3-kinase  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S41053; S54549; S53963  
R/Thomas, S.; Brake, B.; Luzzio, J.P.; Stanley, K.; Banting, G.  
Biochem. Biophys. Acta 1220, 219-222, 1994  
A/Title: Isolation and sequence of a full length cDNA encoding a novel rat inositol 1,4,5-  
A/Reference number: S41053; MUID:94146119; PMID:8312366  
A/Accession: S41053





T42444  
ID=MYO-inositol-triphosphate 3-kinase (EC 2.7.1.127) 1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T42444  
R:Cladding, T.R.; Demodena, J.A.; Sternberg, P.W.  
Cell 92, 523-533, 1998  
A:Title: Inositol triphosphate mediates a Ras-independent response to LFT-23 receptor  
A:Reference number: 222166; MUID:98150857; PMID:9431893  
A:Accession: T42444  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-494 <CLAS>  
A:Molecule type: mRNA  
A:Cross-references: UNIPROT:O45049; UNIPARC:UPI0000076340; EMBL:AF045611; NID:G2898157;  
C:Genetics:  
A:Note: LFB-2  
C:Keywords: phosphotransferase

Query Match 44.3%; Score 321; DB 2; Length 494;  
Best Local Similarity 48.6%; Pred. No. 1.2e-22;  
Matches 67; Conservative 21; Mismatches 48; Indels 2; Gaps 2;  
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DB 319 AITFLRYMQRMTNSTSTLGFRIEIGIKKADGTCNTNFKTQALEQVTKVLEDFVGDHV 60  
QY 61 -IIQKVVACLEELAELEISPFKTHEVVGSSLLFVHDHTGLAKVMIDPEKTVALLPDHQ 119  
DB 379 RVRQQLERLKSMTKALIEHSFNSHEVGSILIVD-TEKVCMMIDFAKSSPVNGR 437  
QY 120 TLSHRLPMAEGNREDGYL 137  
DB 438 TLNRTTWIRGNEDGYL 455

RESULT 10  
T50224  
probable arginine metabolism transcription control protein (imported) - fission yeast (S  
C:Species: Schizosaccharomyces pombe  
C>Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T50224  
R:Zimmermann, W.; Wambut, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, December 1999  
A:Reference number: 225047  
A:Accession: T50224  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-268 <ZIM>  
A:Cross-references: UNIPROT:Q9US14; UNIPARC:UPI000006AE2B; EMBL:AL135751; PIDN:CAB63791.  
A:Experimental source: strain 972h(-); cosmid c607  
C:Genetics:  
A:Gene: SPDB:SPAC607.04  
A:Map position: 1

Query Match 12.4%; Score 90; DB 2; Length 268;  
Best Local Similarity 29.2%; Pred. No. 0.48;  
Matches 40; Conservative 14; Mismatches 43; Indels 40; Gaps 6;  
QY 15 SSTG-TLGFRIEIGIKKADGTCNTNFK-----KTQALEQVTKVLEDFVGDHVIILQKYVA 67  
DB 125 STTSGSLGFRITGLISMTNTNNTYIKRSTANGKTLTDSVVEGLNDF-----FVS 174  
QY 68 C-----LEELRALEISPFKTHEVVGSSLLFVHDHTGLAKVM-----MI 107  
DB 175 CSLGOKARLVESFLNLKLFVNDSESYIELKSSILFVYDSSINLPTFHGESNVVLKLI 234  
QY 108 DFGK---TVALLPDHQT 121  
DB 235 DLASRWTKNTIDHNTL 251

RESULT 11  
T32105

hypothetical protein F45C12.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T32105  
R:Johnson, D.; Kramer, J.; Keppeler, D.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid F45C12.  
A:Reference number: 221123  
A:Accession: T32105  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-555 <JOH>  
A:Cross-references: UNIPROT:O16745; UNIPARC:UPI0000082C77; EMBL:AF016684; PIDN:AAB66215.1  
A:Experimental source: strain Bristol N2; clone F45C12  
C:Genetics:  
A:Gene: CESP:F45C12.5  
A:Map position: 2  
A:Introns: 26/2; 307/3; 375/3; 465/3

Query Match 10.8%; Score 78; DB 2; Length 555;  
Best Local Similarity 23.2%; Pred. No. 15;  
Matches 35; Conservative 25; Mismatches 51; Indels 40; Gaps 8;  
QY 4 KPRYMQRMTNSTSTLGFRIEIGIKKADG-----TCNTNFKK---TQALEQVTKVLEDF 53  
DB 175 KPNVQ-----IVRNLDKFTVNSDGDAGQGLNNMLASNAFIFLKEWTLSSNQINLFLKH 230  
QY 54 FVGDHVIILQKYVACLEELR-----EALIEISPFKTHEVVGSSLLFVHDHT----- 99  
DB 231 WAGSNEMLRGFM--LEQLRAYVQSIENGIDQPSVREHGVKENNLYLPHQKPDIT 288  
QY 100 ---GLAKV--WMIDFGKTVALPDHQTSLRL 125  
DB 289 RNDGMRATFYALGMEQR-----HSSLQRL 314

RESULT 12  
T27707  
hypothetical protein ZK1193.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27707  
R:Geisler, C.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid ZK1193.  
A:Reference number: 220409  
A:Accession: T27707  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-476 <GEI>  
A:Cross-references: UNIPROT:Q23410; UNIPARC:UPI0000073BE9; EMBL:U41553; PIDN:AAA63292.1;  
C:Genetics:  
A:Gene: CESP:ZK1193.3  
A:Introns: 22/3; 132/1; 182/3; 308/1; 358/3; 403/1

Query Match 10.7%; Score 77.5; DB 2; Length 476;  
Best Local Similarity 21.8%; Pred. No. 14;  
Matches 34; Conservative 27; Mismatches 42; Indels 53; Gaps 8;  
QY 18 STLGFRIEIGI-----KKADGTCN---TN-FKKTQALEQVTK----- 49  
DB 199 TTAGFLMEQIVNTRAQILFMITESAGSCNVDAVSTNIFESLRISQLSRGLLIQTSIMQL 258  
QY 50 -----VLEDFVGDHVIILQKYVACLEELRALEISPFKTHEV-----VGSSLLFVHD 97  
DB 259 SDATFSVAQDLMQYDITLND---LEDCRAAPMFQPFVDOSIDFLTLRASGFIIFI-- 312  
QY 98 HTGLAKVMNI--DFGKTVALPDHQTSLRLPMAEGN 131  
DB 313 -----KQNTISANISPIITLPNNTQSLQFLYSND 343

RESULT 13

E70320  
polyribonucleotide nucleosidyltransferase - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #ext\_change 09-Jul-2004  
C:Accession: E70320  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: E70320  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-775 <ACF>  
A:Cross-references: UNIPROT:066593; UNIPARC:UPI00000562CC; GB:AE000679; NID:92982936; PI  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: phpA  
C:Superfamily: polyribonucleotide nucleosidyltransferase

Query Match 10.7%; Score 77.5; DB 2; Length 775;  
Best Local Similarity 26.9%; Pred. No. 26;  
Matches 35; Conservative 23; Mismatches 43; Indels 29; Gaps 7;  
Oy 4 KPRYQWETMSSTSLG---FRIGIKKADGTCNTNPKTQALBQVTK-----VLEDPV 55  
Db 473 KDRYVILSDIIGDEBDHLGDMDFKVGTK--DGI--TSVQMDIKVIGITKEIMLDLKKAR 528  
Oy 56 DGDHYILQKYVACLEELREALISPPFKTHEVY-----GSSLFVHDHTGL 101  
Db 529 EGRYLILKMYEALPEPRK--EPHPTKPEVVDVPEKAPLIGPGSTVKKIYDETGV 586  
Oy 102 AKVMIDFGK 111  
Db 587 -KVMVGEGK 595

RESULT 14  
A12002  
hypotheetical protein alr1575 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: A12002  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritguchi  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tadota, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: A12002  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1047 <KUR>  
A:Cross-references: UNIPROT:08YVNO; UNIPARC:UPI00000CE131; GB:BA000019; PIDN:BA077941.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr1575

Query Match 10.5%; Score 76; DB 2; Length 1047;  
Best Local Similarity 25.2%; Pred. No. 50;  
Matches 32; Conservative 17; Mismatches 44; Indels 34; Gaps 7;

Oy 36 TNPKKT--QALEQYTKVLEDFVDGDHYILQKYVACLEELREALISPPFKT---HEVGS 90  
Db 477 TNFEQETIRGIESANNFL--FIISSKSISSPY--CTTEVEYAMNINKRIIVTLVREIRGA 532  
Oy 91 SLFVHDHTGLAKVMIDFG-----KTVALPDHOTLSH-----RLPMAEG 130  
Db 533 TL-----HPGLAKVQWIDFSGHNTDFLTRFGLTRITLSDPBYVASHTRIFLKKADWEEH 587  
Oy 131 NREDCYL 137  
Db 588 NRDSDFL 594

RESULT 15  
H86391  
hypotheetical protein T1K7.13 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C:Accession: H86391  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: AB6141; MUID:21016719; PMID:11130712  
A:Accession: H86391  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-302 <STO>  
A:Cross-references: UNIPROT:09FZD5; UNIPARC:UPI00000A8E7F; GB:AE005172; NID:9797750; PI  
C:Genetics:  
A:Map position: 1  
C:Superfamily: hypotheetical protein containing F-box domain

Query Match 10.3%; Score 75; DB 2; Length 302;  
Best Local Similarity 30.3%; Pred. No. 15;  
Matches 27; Conservative 11; Mismatches 31; Indels 20; Gaps 5;  
Oy 50 VLEDVVDGDHYILQKYVACLEELREALISPPFKTHEVVGSSSLFVHDHTGLAKW-MID 108  
Db 169 VKSFFGYDPVSDYKSCWTERRRGLQDP--SSEHQVF-----TLSEKKPKWKMD 218  
Oy 109 FGKTVLPDHQTLSHRLPMAEGNREDCYL 137  
Db 219 ---CTSIIDHR-----PMSGVCIDGRV 238

Search completed: May 21, 2006, 04:26:09  
Job time : 40 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein, Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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O9Y475 HUMAN PRELIMINARY; PRT; 604 AA.
ID O9Y475 HUMAN
AC O9Y475;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Inositol 1,4,5-trisphosphate 3-kinase isoenzyme (EC 2.7.1.127)
DE (Fragment).
OS Homo sapiens (Human).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thyroid gland;
RA Takazawa K., Go M., Togaehi S., Endo T., Ernoux C., Onaya T.;
RU Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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EMBL: D8169; BAA2324.1; -; mRNA.
DR Ensembl: ENSG00000086544; Homo sapiens.
DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR005522; IPK.
DR Pfam: PF03770; IPK; 1.
DR Kinase: Transferase. 1
KT NON_PIR 1
SQ SEQUENCE 604 AA; 67236 MW; 52AC5AB5FB3F0176 CRC64;

Query Match 100.0%; Score 725; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 5.4e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVTKPRYQMWRMTSSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 60
DB 452 AVTKPRYQMWRMTSSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 511
OY 61 ILQKYVACLBEALREISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALLPDHOT 120
DB 512 ILQKYVACLBEALREISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALLPDHOT 571
OY 121 LSHRLPWAEGNRDEGYL 137
DB 572 LSHRLPWAEGNRDEGYL 588

RESULT 3
O96DU7 HUMAN PRELIMINARY; PRT; 683 AA.
ID O96DU7 HUMAN
AC O96DU7;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Inositol 1,4,5-trisphosphate 3-kinase C.
GN Name=ITPKC;
OS Homo sapiens (Human).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thyroid;
RA MELIUB=20539819; PubMed=11085927; DOI=10.1042/0264-6021.3520343;
RA DeWaele V., Pouillon V., Moreau C., Shears S., Takazawa K., Ernoux C.;
RT "Cloning and expression of a cDNA encoding human inositol 1,4,5-
RL trisphosphate 3-kinase C."
Biochem. J. 352:343-351(2000).
[2]

```

```

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiński M.I., Skalačka U., Smalls D.E.,
RA Schmeckel A., Schein U.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH WGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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EMBL: AJ290975; CAC40815.1; -; mRNA.
DR Ensembl: BC060788; AAH60788.1; -; mRNA.
DR SMR: Q96DU7; 425-683.
DR Ensembl: ENSG00000086544; Homo sapiens.
DR HGN: HGNC:14897; ITPKC.
DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR InterPro: IPR005522; IPK.
DR Pfam: PF03770; IPK; 1.
KT Kinase.
SQ SEQUENCE 683 AA; 75207 MW; 58093A2A8E046458 CRC64;

Query Match 100.0%; Score 725; DB 2; Length 683;
Best Local Similarity 100.0%; Pred. No. 6.2e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVTKPRYQMWRMTSSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 60
DB 531 AVTKPRYQMWRMTSSTSTLGFRIEIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 590
OY 61 ILQKYVACLBEALREISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALLPDHOT 120
DB 591 ILQKYVACLBEALREISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALLPDHOT 650
OY 121 LSHRLPWAEGNRDEGYL 137
DB 651 LSHRLPWAEGNRDEGYL 667

RESULT 4
Q80ZG2 RAT PRELIMINARY; PRT; 678 AA.
ID Q80ZG2 RAT
AC Q80ZG2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Inositol 1,4,5-trisphosphate 3-kinase C.
GN Name=Itpkc; Synonyms=Ip3k-C;
OS Rattus norvegicus (Rat).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Glires; Rodentia; Sciurognathi;
OC Mammalia; Eutheria; Euarchontoglires;

```

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:17:09 ; Search time 296 Seconds

(without alignments)  
428.132 Million cell updates/sec

Title: US-10-781-581-226

Sequence: 1 AVTFRYVQWETWSTSTL.....HOTLSRLPMAEGNREGYL 137

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trcprot:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	725	100.0	137	Q9UE25_HUMAN	Q9UE25 homo sapien
2	725	100.0	604	Q9Y475_HUMAN	Q9Y475 homo sapien
3	725	100.0	683	Q96DU7_HUMAN	Q96DU7 homo sapien
4	660	91.0	678	Q80ZG2_RAT	Q80ZG2 rattus norv
5	658	90.8	678	Q3U384_MOUSE	Q3U384 mus musculu
6	658	90.8	678	Q7TS72_MOUSE	Q7TS72 mus musculu
7	524	72.3	300	Q4SP10_TETNG	Q4SP10 tetradon n
8	517	71.3	395	Q5RGF8_BRARE	Q5RGF8 brachydantio
9	514	70.9	452	Q9YH86_CHICK	Q9YH86 gallus galli
10	513	70.8	400	Q5XK93_XENLA	Q5XK93 xenopus lae
11	513	70.8	516	Q2TA84_XENLA	Q2TA84 xenopus lae
12	507	69.9	325	Q4SC34_TETNG	Q4SC34 tetradon n
13	506	69.8	425	Q4RM63_TETNG	Q4RM63 tetradon n
14	506	69.8	455	IP3KA_MOUSE	IP3KA mus musculu
15	506	69.8	459	IP3KA_HUMAN	IP3KA homo sapien
16	504	69.5	461	IP3KA_RAT	IP3KA rattus norv
17	496.5	68.5	298	Q8JFJ9_BRARE	Q8JFJ9 brachydantio
18	494.5	68.2	195	Q2TUE8_HUMAN	Q2TUE8 homo sapien
19	493	68.0	472	Q2TUE8_HUMAN	Q2TUE8 homo sapien
20	493	68.0	472	Q2TUE8_HUMAN	Q2TUE8 homo sapien
21	487	67.2	934	IP3KB_HUMAN	IP3KB homo sapien
22	442	61.0	310	Q4S868_TETNG	Q4S868 tetradon n
23	434	59.9	282	Q73592_CHICK	Q73592 gallus galli
24	410.5	56.6	377	Q5TX95_ANOGA	Q5TX95 anopheles g
25	410.5	56.6	377	Q5TX95_ANOGA	Q5TX95 anopheles g
26	403.5	55.7	669	Q8XSX8_DROME	Q8XSX8 drosophila
27	403.5	55.7	669	Q8XSX8_DROME	Q8XSX8 drosophila
28	387	53.4	463	Q963D4_ARIME	Q963D4 apis mellif
29	387	53.4	463	Q963D4_ARIME	Q963D4 apis mellif
30	387	53.4	463	Q963D5_ARIME	Q963D5 apis mellif
31	321	44.3	393	Q61HCS_CAEEL	Q61HCS caenorhabdi

32	321	44.3	394	2	Q45050_CAEEL	Q45050 caenorhabdi
33	321	44.3	394	2	Q95063_CAEEL	Q95063 caenorhabdi
34	321	44.3	461	2	Q45051_CAEEL	Q45051 caenorhabdi
35	321	44.3	461	2	Q9GY16_CAEEL	Q9GY16 caenorhabdi
36	321	44.3	494	2	Q45048_CAEEL	Q45048 caenorhabdi
37	321	44.3	494	2	Q95062_CAEEL	Q95062 caenorhabdi
38	316.5	43.7	308	2	Q5DHU6_SCHJA	Q5DHU6 schistosoma
39	259.5	35.8	441	2	Q95R55_DROME	Q95R55 drosophila
40	259.5	35.8	441	2	Q9VL83_DROME	Q9VL83 drosophila
41	246.5	34.0	305	2	Q7Q1X4_ANOGA	Q7Q1X4 anopheles g
42	129	17.8	172	2	Q9PM03_CHICK	Q9PM03 gallus galli
43	129	17.8	181	2	Q9PM02_CHICK	Q9PM02 gallus galli
44	90	12.4	268	2	Q9US14_SCHPO	Q9US14 schizosacch
45	86	11.9	569	2	Q2R2E6_ORYSA	Q2R2E6 oryza sativ

## ALIGNMENTS

## RESULT 1

Q9UE25\_HUMAN PRELIMINARY; PRT; 137 AA.

AC Q9UE25\_01-MAY-2000, integrated into UniprotKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DE 07-FEB-2006, entry version 15.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RC NUCLEOTIDE SEQUENCE.

RP TISSUE=Placenta;

RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

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CC EMBL; Y1199; CAAT2728.1; -; mRNA.

DR SRR; Q9UE25; 1-137.

DR Ensembl; ENSG00000086544; Homo sapiens.

DR LinkHub; Q9UE25; -.

DR GO; GO:0008440; P:inositol triphosphate 3-kinase activity; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.

DR InterPro; IPR005522; IPK; 1.

DR Pfam; PF03770; IPK; 1.

DR KINASE.

FT NON\_TER

FT 137

FT 137

FT 137

FT 137

SEQUENCE 137 AA; 15596 MW; C8D48FC6D2AE40A CRC64;

Query Match 100.0%; Score 725; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 1e-60;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTFRYVQWETWSTSTLGFRIEIKKADGTCNTNPFKKTQALEQYTKVLEDFVDDGV 60

DB 1 AVTFRYVQWETWSTSTLGFRIEIKKADGTCNTNPFKKTQALEQYTKVLEDFVDDGV 60

QY 61 ILQRYVACLEELRALISPEFKTHEVVGSSILFVHDHTGLAKRMIDFGTVALPHQT 120

DB 61 ILQRYVACLEELRALISPEFKTHEVVGSSILFVHDHTGLAKRMIDFGTVALPHQT 120

QY 121 LSHRLPMAEGNREGYL 137

DB 121 LSHRLPMAEGNREGYL 137

QY 121 LSHRLPMAEGNREGYL 137

DB 121 LSHRLPMAEGNREGYL 137

RESULT 2





RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirokane K., Shikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arahata T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=21055660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arahata T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,  
 RA Hayashizaki Y.,  
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 RL Nature 409:685-690 (2001).  
 [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama Y., Nishi K., Kitahara T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwaigi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ND;  
 RA Arahata T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
 RA Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,  
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,  
 RA Nishiyori H., Nomura K., Ono M., Sakazume N., Sano H., Saeki D.,  
 RA Shibata K., Shiraki T., Tagami Y., Tagami Y., Waki K., Watanuki A.,  
 RA Muramatsu M., Hayashizaki Y.,  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; AK154888; BAB32904.1; -, mRNA.

DR MGI:2442554; Itpkc.  
 DR GO:0008440; F:inositol triphosphate 3-kinase activity; IDA.  
 DR InterPro: IPR005522; IPK.  
 DR Pfam: PF03770; IPK; 1.  
 DR KInase.  
 SQ SEQUENCE 678 AA; 74492 MW; 61DFCB3F3CC6B807 CRC64;  
 Query Match 90.8%; Score 658; DB 2; Length 678;  
 Best Local Similarity 91.2%; Pred. No. 1,4e-53;  
 Matches 125; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 AVTKPRYMQWRETMSSTSLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVNDGHV 60  
 DB 526 AITKPRYMQWRETSLSTSLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVNDGLG 585  
 QY 61 ILQKYACIEELREALIEPFFKTHFVVGSSLLFVNDHGLAKVMWIDGKTVLAPDHQT 120  
 DB 586 ILRKVYARLEDLRETLNENPFFKTHFVVGSSLLFVNDHGLAKVMWIDGKTVLAPDHQW 645  
 QY 121 LSHRLPMAGNREDGYL 137  
 DB 646 LSHRLPMAGNREDGYL 662  
 RESULT 6  
 ID 07TS72\_MOUSE PRELIMINARY; PRT; 678 AA.  
 AC 07TS72;  
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Inositol 1,4,5-trisphosphate 3-kinase C.  
 GN Name=Itpkc;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Limb;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueidi T.B., Tothiyuki S., Carninci P., Muliyil S.J.,  
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Vallier J., Halton E., Kettman M., Madan A., Rodriguez Y., Bouffard G.G.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Limb;  
 RA Strausberg R.,  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; BC053450; AAH53450.1; -, mRNA.  
 DR SMR; 07TS72; 420-678.

DR Ensemble; ENSMUSG0000003752; Mus musculus.  
DR MGI; MGI:2442554; Itpkc.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IDA.  
DR InterPro; IPR005522; IPK.  
DR Pfam; PF03770; IPK; 1.  
KW Kinase.  
SQ SEQUENCE 678 AA; 74493 MW; 0D3705B3D682BED CRC64;  
Query Match 90.8%; Score 658; DB 2; Length 678;  
Best Local Similarity 91.2%; Pred. No. 1.4e-53;  
Matches 125; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AVTKRYVMQREMTSSTSLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDH 60  
Db 526 AITKRYVMQREMTSSTSLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDH 585  
QY 61 ILQKYVACLEBELREALISPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALPDHQT 120  
Db 586 ILKRYVACLEBELREALISPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALPDHQM 645  
QY 121 LSHRLPWAEGNRDEGYL 137  
Db 646 LSHRLPWAEGNRDEGYL 662  
RESULT 7  
Q4SPLO\_TESTNG PRELIMINARY; PRT; 300 AA.  
ID Q4SPLO\_TESTNG  
AC Q4SPLO\_TESTNG  
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE Chromosome 16 SCAP14537, whole genome shotgun sequence. (Fragment).  
GN ORFNames=STENG0001479001.  
OS Tetradon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15496914; DOI=10.1038/nature03025;  
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,  
RA Nicard S., Jaffe D., Fisher S., Lutfella G., Dossat C., Segurens B.,  
RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Aichmond V., Jabin C., Catellico L., Poullain J., De Bernardis V.,  
RA Crnaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,  
RA Parra G., Lardier G., Chappe C., McKernan K.J., McMan P., Boeak S.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landet V., Schachter V., Queller F., Saurin W., Scarpetelli C.,  
RA Winkler P., Lander B.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals  
the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC  
CC EMBL; CA001014537; CAF97422.1; -; Genomic DNA.  
DR SNR; Q4SPLO; 40-295.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
FT NON\_TER 1 1

SQ SEQUENCE 300 AA; 34775 MW; 5E32D39B508A7EF CRC64;  
Query Match 72.3%; Score 524; DB 2; Length 300;  
Best Local Similarity 72.8%; Pred. No. 3.1e-41;  
Matches 99; Conservative 14; Mismatches 23; Indels 0; Gaps 0;  
QY 2 VTKRYVMQREMTSSTSLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDH 61  
Db 147 ILKRYVMQREMTSSTSLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDH 206  
QY 62 LQKYVACLEBELREALISPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALPDHQT 121  
Db 207 LKLYVORLQIRSVLEQSFQTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALPDHQT 266  
QY 122 LSHRLPWAEGNRDEGYL 137  
Db 267 LSHRLPWAEGNRDEGYL 282  
RESULT 8  
Q5RGF8\_BRARE PRELIMINARY; PRT; 395 AA.  
ID Q5RGF8\_BRARE  
AC Q5RGF8\_BRARE  
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.  
DT 21-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Novel protein similar to vertebrate inositol 1,4,5-trisphosphate 3-  
DE kinase B (ITPKB) (Fragment).  
GN Name=OTTDARP0000006972; ORFNames=CH211-235J18.1-001;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Donaldson S.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Dyer L.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
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CC  
CC EMBL; BX649588; CA111856.1; JOINED; Genomic DNA.  
DR EMBL; BX901888; CA111856.1; -; Genomic DNA.  
DR EMBL; BX649588; CA112065.1; -; Genomic DNA.  
DR EMBL; BX901888; CA112065.1; JOINED; Genomic DNA.  
DR SNR; Q5RGF8; 120-389.  
DR Ensemble; ENSDARG00000010059; Danio rerio.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR InterPro; IPR005522; IPK.  
DR Pfam; PF03770; IPK; 1.  
KW Kinase.  
FT NON\_TER 1 1  
SQ SEQUENCE 395 AA; 45081 MW; 7FDA7607A5D0433 CRC64;  
Query Match 71.3%; Score 517; DB 2; Length 395;  
Best Local Similarity 71.5%; Pred. No. 1.9e-40;  
Matches 98; Conservative 14; Mismatches 25; Indels 0; Gaps 0;  
QY 1 AVTKRYVMQREMTSSTSLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDH 60  
Db 240 AITKRYVMQREMTSSTSLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDH 299  
QY 61 ILQKYVACLEBELREALISPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALPDHQT 120  
Db 300 ILKRYVACLEBELREALISPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALPDHQM 359  
QY 121 LSHRLPWAEGNRDEGYL 137

DB 360 LSHRATMEGREDGYL 376

|||||

RESULT 9

Q9YH86 CHICK PRELIMINARY; PRT; 452 AA.

ID Q9YH86 CHICK PRELIMINARY; PRT; 452 AA.

AC Q9YH86

DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 1.

DE Ip3ka protein (EC 2.7.1.127).

GN Name=ip3ka;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=9173870; PubMed=1072759; DOI=10.1016/S0378-1119(99)00018-9; RA Bertsch U., Haefl M., Moeller M., Deschermelier C., Fanick W., RA Kitzrow A., Ozaki S., Meyer H.E., Mayr G.W.; RT "A novel A-isoform-like inositol 1,4,5-trisphosphate 3-kinase from RT chicken erythrocytes exhibits alternative splicing and conservation of RT intron positions between vertebrates and invertebrates."; RL Gene 228:61-71(1999).

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CC EMBL: AJ012219; CA09965.1; -; mRNA.

DR SMR: Q9YH86; 179-452.

DR EMBL: ENSGALG00000008603; Gallus gallus.

DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IEA.

DR GO: GO:0016740; F:transferase activity; IEA.

DR InterPro: IPR005522; IPK.

DR Pfam: PF03770; IPK; 1.

DR Transferase 452 AA; 51097 MW; FABA67971A7B6CC CRC64;

SQ SEQUENCE

Query Match 70.9%; Score 514; DB 2; Length 452;

Best Local Similarity 70.1%; Pred. No. 4.3e-40;

Matches 96; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 AVTPTPTMPTMTSTSTLTGFRLEGIKKADGTCTNPFKTKTQALEQVTKLQEDVVDGHHV 60

DB 300 AVTPTPTMPTMTSTSTLTGFRLEGIKKADGTCTNPFKTKTQALEQVFEPIEGVTT 359

QY 61 ILQKYVACLEIRALEISPPFKTHEVYVSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 120

DB 360 ILKRYLVRLKRLKLEIRALEISPPFKTHEVYVSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 419

QY 121 LSHRLPMAEGNRREDGYL 137

DB 420 LSHRLPMAEGNRREDGYL 436

RESULT 10

Q5XK93 XENLA PRELIMINARY; PRT; 400 AA.

ID Q5XK93 XENLA PRELIMINARY; PRT; 400 AA.

AC Q5XK93

DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.

DT 23-NOV-2004, sequence version 1.

DE LOC494865 protein (Fragment).

GN Name=LOC494865;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; OC Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., RA Richardson P.; RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT Initiative"; RL Dev. Dyn. 225:384-391(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E., RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Mullahy S.J., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E., RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."; RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;

RA Klein S., Gerhardt D.S.; RT Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

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CC EMBL: BC083019; AAH83019.1; -; mRNA.

DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IEA.

DR InterPro: IPR005522; IPK.

DR Pfam: PF03770; IPK; 1.

FT NON\_TER 1

SQ SEQUENCE 400 AA; 45383 MW; 6F0D464A2BFA4874 CRC64;

Query Match 70.8%; Score 513; DB 2; Length 400;

Best Local Similarity 70.8%; Pred. No. 4.7e-40;

Matches 97; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 1 AVTPTPTMPTMTSTSTLTGFRLEGIKKADGTCTNPFKTKTQALEQVTKLQEDVVDGHHV 60

DB 248 AVTPTPTMPTMTSTSTLTGFRLEGIKKADGTCTNPFKTKTQALEQVTKLQEDVVDGHHV 307

QY 61 ILQKYVACLEIRALEISPPFKTHEVYVSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 120

DB 308 ILKRYLVRLKRLKLEIRALEISPPFKTHEVYVSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 367

QY 121 LSHRLPMAEGNRREDGYL 137

DB 368 LSHRLPMAEGNRREDGYL 384

RESULT 11

Q2TAE4 XENLA PRELIMINARY; PRT; 516 AA.

ID Q2TAE4 XENLA PRELIMINARY; PRT; 516 AA.

AC Q2TAE4

DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.

DT 24-JAN-2006, sequence version 1.

DE LOC494865 protein (Fragment).

GN Name=LOC494865;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; OC Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 NCBI\_TaxId=8355;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Straubeberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Wozniak K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Fahy J., Helton E., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallos D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Klein S., Gernard D.S.,  
 RL Submitted (DEC-2005) to the EMBL/Genbank/DBJ databases.  
 CC -----  
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 CC -----  
 CC EMBL; BC110967; AAI10968.1; -; mRNA.  
 DR KW Hypothetical protein.  
 SQ SEQUENCE 516 AA; 58271 MW; 2693D817D8AD957A CRC64;  
 QY Query Match 70.8%; Score 513; DB 2; Length 516;  
 Db Beut Local Similarity 70.8%; Pred. No. 6.3e-40;  
 Matches 97; Conservative 17; Mismatches 23; Indels 0; Gaps 0;  
 QY 1 AVTKRYVQWMEPTWSTSLGFRIGIKKADGTCTNPKTKQALQVTKVLEDVFDGSHV 60  
 Db 364 AILKPRYQWMEPTWSTSLGFRIGIKKADGTCTNPKTKCKQVLSALNPFVDSKN 423  
 QY 61 ILQKTVACLEBRLAEISPFKTEHVGVSSLLFVHDHTGLAKVMWIDFGKVALPDHOTL 120  
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 QY 121 LSHRLPMAEGNREDGYL 137  
 Db 484 LNHRTPWEGNREDGYL 500

DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
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 GN ORFNames=GSTENG00020685001;  
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 RN NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jallón O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
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 RA Nicod S., Jaffe D., Fisher S., Laitalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castel V., Katink M., Vacherie B.,  
 RA Bismont C., Skallil Z., Catcolico L., Poulain J., De Bernardis V.,  
 RA Chaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan F., Bosak S.,  
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Queller F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957 (2004).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.  
 CC -----  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -----  
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 CC -----  
 CC EMBL; CAE01014660; CAG01798.1; -; Genomic DNA.  
 DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
 FT NON TER 1 1  
 FT NON TER 325 325  
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 QY Query Match 69.9%; Score 507; DB 2; Length 325;  
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 Matches 94; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
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 Db 237 LKCTLSRLAEIRDLTEISPFKAHVGVSSLLFVHDSIGRAKVMWIDFGKTPAPDGBEL 296  
 QY 122 LSHRLPMAEGNREDGYL 137  
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 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
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 RX PubMed=15496914; DOI=10.1038/nature03025;  
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 RA Anthouard V., Jabin C., Castellani V., Kacinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cactolico L., Poullain J., De Berardinis V.,  
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 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Landel V., Schachter V., Queller F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RG Genoscope, Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC EMBL: CA601015019; CAG10519.1; -; Genomic DNA.  
 DR GO: GO:0008440; P:inositol triphosphate 3-kinase activity; IEA.  
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 Query March 69.8%; Score 506; DB 2; Length 425;  
 Best Local Similarity 66.9%; Pred. No. 2.3e-39;  
 Matches 91; Conservative 23; Mismatches 22; Indels 0; Gaps 0;  
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 QY 62 LQKTVACLEERLEALISPPFKTHEVVGSSLLFVHDHTGLAKRMWIDFGKVALPDHOTL 121  
 DB 335 IKSYSRLREIQRALKKSAFPKQHEVIGSSLLFHDHTGKAQWVIDFGKTTALPEGOTL 394  
 QY 122 SHRLPWAEGNREDGYL 137  
 DB 395 KHDVPMQEGNREDGYL 410  
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 IP3KA MOUSE STANDARD; PRT; 459 AA.  
 AC Q8R071; integrated into UniProtKB/Swiss-Prot.  
 DT 19-JUN-2004, sequence version 1.  
 DT 01-JUN-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 18.  
 DE Inositol-tri-phosphate 3-kinase A (EC 2.7.1.127) (inositol 1,4,5-  
 DE triphosphate 3-kinase A) (IP3K A) (IP3 3-kinase A).  
 GN Name:ItpkA;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
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 RP NOCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Cantici P., Prange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Motley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- CATALYTIC ACTIVITY. ATP + 1D-myo-inositol 1,4,5-trisphosphate =  
 CC ADP + 1D-myo-inositol 1,3,4,5-tetrakisphosphate  
 CC -1- ENZYME REGULATION. IP3K is activated by calmodulin (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the inositol phosphokinase (IPK) family.  
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 CC EMBL: BC027291; AA87291.1; -; mRNA.  
 DR SNR; Q8R071; 185-459.  
 DR InFect; Q8R071; -;  
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 DR MGI; MGI:1333822; ItpkA.  
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 DR GO: GO:0006020; P:myo-inositol metabolism; IMP.  
 DR InterPro; IPR005522; IPK.  
 DR Pfam; PF03770; IPK; 1.  
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 FT BINDING 207 207 ATP (By similarity).  
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 FT BINDING 262 262 Substrate (By similarity).  
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 Best Local Similarity 67.2%; Pred. No. 2.5e-39;  
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 QY 1 AVTKPRYQMRETWSTSTLTGFRIGIKKADGTCNTNFKKQALDEQVTKVLEDFVGDHVI 60  
 DB 307 AVTKPRYQMRETWSTSTLTGFRIGIKKADGTCNTNFKKQALDEQVTKVLEDFVGDHVI 366  
 QY 61 ILQKTVACLEERLEALISPPFKTHEVVGSSLLFVHDHTGLAKRMWIDFGKVALPDHOTL 120  
 DB 367 VLRLYLRQLQRIITLISDFRRHEVIGSSLLFVHDHCHRAQWVIDFGKTTALPEGQI 426  
 QY 121 LSHRLPWAEGNREDGYL 137  
 DB 427 LDHRRPWEQGNREDGYL 443



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 DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1991, sequence version 3.  
 DE 07-FEB-2006, entry version 42.  
 DE Inositol-trisphosphate 3-kinase A (EC 2.7.1.127) (inositol 1,4,5-  
 DE trisphosphate 3-kinase A) (IP3K A) (IP3 3-kinase A).  
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 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
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 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RX MEDLINE=91090700; PubMed=2176078;  
 RA Takazawa K., Vandekerckhove J., Dumont J.E., Erneux C.;  
 RT "Cloning and expression in Escherichia coli of a rat brain cDNA  
 RT encoding a Ca<sup>2+</sup>/calmodulin-sensitive inositol 1,4,5-trisphosphate 3-  
 RT kinase.";  
 RL Biochem. J. 272:107-112(1990).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=90208336; PubMed=2157285;  
 RA Choi K.Y., Kim H.K., Lee S.Y., Moon K.H., Sim S.S., Kim J.W.,  
 RA Chung H.K., Rhee S.G.;  
 RT "Molecular cloning and expression of a complementary DNA for inositol  
 RT 1,4,5-trisphosphate 3-kinase.";  
 RL Science 248:64-66(1990).  
 RN [3]  
 RP PROTEIN SEQUENCE OF 315-326, AND ACTIVE SITE.  
 RX MEDLINE=95374430; PubMed=7646431;  
 RA Communi D., Lecocq R., Vanweyenbergh V., Erneux C.;  
 RT "Active site labelling of inositol 1,4,5-trisphosphate 3-kinase A by  
 RT phenylglyoxal.";  
 RL Biochem. J. 310:109-115(1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 185-459 IN COMPLEX WITH ADP.  
 RX PubMed=15350215; DOI=10.1016/j.molcel.2004.08.005;  
 RA Miller G.J., Hurley J.H.;  
 RT "Crystal structure of the catalytic core of inositol 1,4,5-  
 RT trisphosphate 3-kinase.";  
 RL Mol. Cell 15:703-711(2004).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1D-myo-inositol 1,4,5-trisphosphate =  
 CC ADP + 1D-myo-inositol 1,3,4,5-tetrakisphosphate.  
 CC -1- ENZYME REGULATION: IP3K is activated by calmodulin.  
 CC -1- SIMILARITY: Belongs to the inositol phosphokinase (IPK) family.  
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 CC -----  
 CC EMBL: X56917; CAA40248.1; -, mRNA.  
 DR EMBL: M29787; AAA41457.1; ALT\_INIT; mRNA.  
 DR PIR: S13064; S13064.  
 DR PDB: 1TZD; X-ray; A/B=185-459.  
 DR Ensembl: ENSRNOG0000005284; Rattus norvegicus.  
 DR RGD: 619950; Itcpka.  
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 DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IDA.  
 DR InterPro: IPR005522; IPK.  
 DR Pfam: PF03770; IPK. 1  
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 FT REGION 310 317  
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 Best Local Similarity 67.2%; Pred. No. 2.5e-39;  
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 Oy 1 AVTTPRMQREMTSSTSTGFRLEGKKADGTNTNFKTKQALQVTKLEDFVGDHV 60  
 Db 307 AVTTPRMQREMTSSTSTGFRLEGKKADGTNTNFKTKQALQVTKLEDFVGDHV 366  
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 Db 367 VLKRYLNRLOQIRITLSDPFRHREYIGSSLLFVHDHCRAGVWLIDPGKTTLPDGOI 426  
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 Db 427 LDHRRPWEENREDGYL 443



Mon May 22 09:43:34 2006

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Page 10

Search completed: May 21, 2006, 04:25:26  
Job time : 299 secs

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: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CLO01107
:
: CURRENT APPLICATION NUMBER: US/09/949,016
:
: PRIOR APPLICATION NUMBER: 2000-04-14
:
: PRIOR FILING DATE: 2000-10-20
:
: PRIOR APPLICATION NUMBER: 60/241,755
:
: PRIOR FILING DATE: 2000-10-20
:
: PRIOR FILING DATE: 2000-10-03
:
: PRIOR APPLICATION NUMBER: 60/237,768
:
: PRIOR FILING DATE: 2000-09-08
:
: PRIOR FILING DATE: 2000-09-08
:
: NUMBER OF SEQ ID NOS: 207012
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 6194
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: LENGTH: 472
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: TYPE: prt
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: ORGANISM: Human
:
: US-09-949-016-6194

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QY 61 ILQKVVACIEELREALIEISPPFKTHVVGSSLLFVHDHTGLAKVMNIDFGKTAALPDHOT 120
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QY 121 LSHRLPMWAGNREDGYL 137
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RESULT 3
US-09-949-016-8219
; Sequence 8219, Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8219
; LENGTH: 504
; TYPE: prt
; ORGANISM: Human
US-09-949-016-8219

```

Query Match	68.0%	Score	493	DB 2	Length	504			
Best Local Similarity	67.9%	Pred. No.	1.8e-50						
Matches	93	Conservative	14	Mismatches	30	Indels	0	Gaps	0

QY            AATKRYWOMREMTSTLTGPIBEIKKADGCGINFPKTOALBVTYKVLBEFVVDGHH 60  
DB            348 AATKRYWOMRETIISTATLTGPIBEIKKEDGVNNDPCKTKRREVTEAFREFTGNIN 407  
QY            61 IIOKVACLBELREALIEIPFFTHAVGSSSLFVHDHGLAVMMIDPGKVALDHQOT 120  
DB            408 IIAIARDRIKARTILEVSPFFKCHEVIGSSSLFIHDKKEQAAVMMIDEGKTPPLREGOT 467  
QY            121 LSHRLPMWAGNREDGYL 137

Db 468 LQHDVPMQEGNREDGYL 484

RESULT 4  
US-09-270-767-33291  
; Sequence 33291, Application US/09270767

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33291
;
; LENGTH: 397
;
; TYPE: PRT
;
; ORGANISM: Drosophila melanogaster
US-09-270-767-33291

```

Query Match	55.7%	Score 403.5; DB 2	Length 397;
Best Local Similarity	56.9%	Pred. No. 7.6e-40;	
Matches 78; Conservative	19;	Mismatches 39;	Indels 1; Gaps 1.

```
QY 1 AVTKRVMQWEPMTMSTILGRIGIKKAQDCTMNEKKQTALBQVTKVLDFVYGDHY 60
Db 211 AVTKRVMYWRBTISTATILGRIGIKKSDSTSSDFTTYSRQIKALFLEBSGHPH 270
QY 61 ILQKVACLEBELREALBETSPFKTHEVWGSSLLFVHDHTGLAKVMWIDFGKTVALBDHOT 120
Db 271 ILPRITQRRARATLAVSEFPQTHEVIGSSLLFVHDTH-ASIWLDPAKTVELPEPQUR 329
QY 121 LSHRLPMAEGNREDGYL 137
Db 330 IDHSAMKVGXNHEDGYL 346
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RESULT 5
US-09-2770-767-48508
; Sequence 48508, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48508
; LENGTH: 397
; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-2770-767-48508

```

Query Match	55.7%	Score 403.5	DB 2	Length 397
Best Local Similarity	56.9%	Pred. No. 7.6e-40		
Matches	78	Conservative 19	Mismatches 39	Indels 1
				Gaps 1

QY 1 AATKRRYQWMBRTMSSTSLGFRIGIKKADGTCNNFEKKQALBOVTYKLBDFVYGDH 60  
 DB 211 AATKRRYQWMBRTMSSTSLGFRIGIKKADGTCNNFEKKQALBOVTYKLBDFVYGDH 270  
 QY 61 ILQKVVACLBELBALETSPEFKTEHVYSSLLFVNDHGLKAWMIDFGKVALPDHOT 120  
 DB 271 ILPRYIQRRARATLAIVSEFQTEHVIGSSLLFVNDH-ASIWLDFAKTVLEPPQLR 329  
 QY 121 LSHRLPMALGNREDGYL 137  
 DB 330 IDHYSAMKGVNHDGYL 346

RESULT 6  
US-09-107-532A-6615  
; Sequence 6615, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6615:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 390 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...390  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6615:  
US-09-107-532A-6615  
Query Match 10.3%; Score 74.5; DB 2; Length 390;  
Best Local Similarity 29.7%; Pred. No. 2.9;  
Matches 33; Conservative 10; Mismatches 31; Indels 37; Gaps 5;  
QY 37 NFKKQALAEVTK-----VLDFVDGHDVHIIQKTVACCELRLEALISPFKTH 85  
DB 190 DFKLSVLENDYKREKVALTEBOQALSLFKTDVNVHKYDDMLILKTGLRIS----- 243  
QY 86 EVVGSLLFVHDHTGLAKVMIDFGKTVALPDHQTLSHRLPMAEGNREDY 136  
DB 244 ELGCG---LTVAD-----IDFKNEVLIIDHQLK-----NKGQY 274  
RESULT 7  
US-09-543-681A-4637  
; Sequence 4637, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709,1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 4637  
; LENGTH: 817  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-4637  
Query Match 10.0%; Score 72.5; DB 2; Length 817;  
Best Local Similarity 25.2%; Pred. No. 15;  
Matches 28; Conservative 21; Mismatches 31; Indels 31; Gaps 5;  
QY 40 KTOALEQVTKVLEDFVDGHDVHIIQKTV-----ACLEEL--REALISPFK 83  
DB 260 KTDALNGVKVYIKH-----DVLNKKYITGINNGKSQGEVYSLVEQLNDKESITISQYND 315  
QY 84 THEVGSLLFVHDHTGLAKVMIDFGKTVALPDHQTLSHRLPMAEGNRED 134  
DB 316 IRAFFGISAFHLSQNIQVSAFLNFAKTHAL-----TISK-----NKOD 355  
RESULT 8  
US-09-949-016-10918  
; Sequence 10918, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10918  
; LENGTH: 2141  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10918  
Query Match 9.8%; Score 71; DB 2; Length 2141;  
Best Local Similarity 21.6%; Pred. No. 88;  
Matches 35; Conservative 20; Mismatches 53; Indels 54; Gaps 5;  
QY 8 MOWRET-----MSTSTIGFRLEGIKKADGTNTNF-----KKTQ 42  
DB 1920 LSWMESTIROIETOERPRDVSVELMKYHGINAEITFSKNFSACLBIGESILQRHQ 1979  
QY 43 ALBOVTKVLEDFVDGHDVHIIQKTVACCELRLEALISPFKTHEVVGSSLLFVHDHTGLA 102  
DB 1980 ASEIEIKKQVWRSRKNEMKEARERKMLLEVCQPSRDSV-----A 2025  
QY 103 KVMYI-----DFKTVALPDHQTLSHRLPMAE 129  
DB 2026 EAWLIAQEPYLAGDFGHTVDSVEKLKHEAFKSTASWAE 2067  
RESULT 9  
US-10-104-047-3353  
; Sequence 3353, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE

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/ TITLE OF INVENTION: No. 6943241e1 full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3353
/ LENGTH: 274
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-104-047-3353

Query Match
Best Local Similarity 36.1%; Score 70; DB 2; Length 274;
Matches 22; Conservative 11; Mismatches 20; Indels 8; Gaps 2;

QY 23 RIEG---IKKADGTGNTNFKKTQALEQVTKLEDFVGDHVLQKVVACLEELREALEI 78
Db 74 RIEGKBEIRADLCRLMKEXLEBEENLTRELKSEIER---LQKRMALFKLEAFSR 129

QY 79 S 79
Db 130 S 130

RESULT 10
US-09-315-127-8
/ Sequence 8, Application US/09315127
/ Patent No. 6448390
/ GENERAL INFORMATION:
/ APPLICANT: The University of Tennessee, c/o Richard Cox
/ TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
/ FILE REFERENCE: 44137-5023, U. of Tennessee
/ CURRENT APPLICATION NUMBER: US/09/315,127
/ CURRENT FILING DATE: 1999-05-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 8
/ LENGTH: 645
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ US-09-315-127-8

Query Match
Best Local Similarity 29.2%; Score 70; DB 2; Length 645;
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETWSTSTL---GFRIGIKKADGTGNTNFKKTQALEQVTKLE---DFVGDHVLQK 64
Db 449 REPVSLTALLGLGTWGIAGIGTGTALTALIKTQDFQLAAIQTDLNEVEKSTINLEK 508

QY 65 YVACLEEL---REALEISPFKTHEVGS---SLFVHDHTGLAK 103
Db 509 SLTSLSEVVLQNRRLDGLL-FLKEGGLCAALKECCFYADHTGLVR 553

RESULT 11
US-09-315-127-9
/ Sequence 9, Application US/09315127
/ Patent No. 6448390
/ GENERAL INFORMATION:
/ APPLICANT: The University of Tennessee, c/o Richard Cox
/ TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
/ FILE REFERENCE: 44137-5023, U. of Tennessee
/ CURRENT APPLICATION NUMBER: US/09/315,127
/ CURRENT FILING DATE: 1999-05-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ US-09-315-127-9
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/ LENGTH: 645
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: SEQ. ID NO.
/ OTHER INFORMATION: 6, envelope protein produced by retroviral vector
/ OTHER INFORMATION: of seq. id no. 5
/ US-09-315-127-9

Query Match
Best Local Similarity 29.2%; Score 70; DB 2; Length 645;
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETWSTSTL---GFRIGIKKADGTGNTNFKKTQALEQVTKLE---DFVGDHVLQK 64
Db 449 REPVSLTALLGLGTWGIAGIGTGTALTALIKTQDFQLAAIQTDLNEVEKSTINLEK 508

QY 65 YVACLEEL---REALEISPFKTHEVGS---SLFVHDHTGLAK 103
Db 509 SLTSLSEVVLQNRRLDGLL-FLKEGGLCAALKECCFYADHTGLVR 553

RESULT 12
US-09-315-127-11
/ Sequence 11, Application US/09315127
/ Patent No. 6448390
/ GENERAL INFORMATION:
/ APPLICANT: The University of Tennessee, c/o Richard Cox
/ TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
/ FILE REFERENCE: 44137-5023, U. of Tennessee
/ CURRENT APPLICATION NUMBER: US/09/315,127
/ CURRENT FILING DATE: 1999-05-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 654
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ US-09-315-127-11

Query Match
Best Local Similarity 29.2%; Score 70; DB 2; Length 654;
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETWSTSTL---GFRIGIKKADGTGNTNFKKTQALEQVTKLE---DFVGDHVLQK 64
Db 458 REPVSLTALLGLGTWGIAGIGTGTALTALIKTQDFQLAAIQTDLNEVEKSTINLEK 517

QY 65 YVACLEEL---REALEISPFKTHEVGS---SLFVHDHTGLAK 103
Db 518 SLTSLSEVVLQNRRLDGLL-FLKEGGLCAALKECCFYADHTGLVR 562

RESULT 13
US-09-315-127-12
/ Sequence 12, Application US/09315127
/ Patent No. 6448390
/ GENERAL INFORMATION:
/ APPLICANT: The University of Tennessee, c/o Richard Cox
/ TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
/ FILE REFERENCE: 44137-5023, U. of Tennessee
/ CURRENT APPLICATION NUMBER: US/09/315,127
/ CURRENT FILING DATE: 1999-05-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 654
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: SEQ. ID NO.
```

OTHER INFORMATION: 8, envelope protein produced by retroviral vector  
OTHER INFORMATION: of seq. id no. 7  
US-09-315-127-12

Query Match 9.7%; Score 70; DB 2; Length 654;  
Best Local Similarity 29.2%; Pred. No. 21;  
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETMSTSTL--GPRIGIKKADGTGNTNFKKQALQVTVKLE---DFVNGDHVILQK 64  
DB 458 REPVSLLTALLGTLGTMGIALGIGTALIKTQGFQDLHAIDQLNEVKSITNLEK 517  
QY 65 YVACLEEL---REALISPFKTHVWGS---SLFVHDHTGLAK 103  
DB 518 SLTSLSEVVLQNRRLDLDL-FLKEGGLCALKECCCFADHTGLVR 562

RESULT 14  
US-08-844-086-2  
Sequence 2, Application US/08844086  
Patent No. 5866390

GENERAL INFORMATION:  
APPLICANT: Lawlor, Elizabeth  
TITLE OF INVENTION: No. 5866390e1 Compounds  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA

COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,086  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9607993.4  
FILING DATE: 18-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimm, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P31457-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 833 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-844-086-2

Query Match 9.6%; Score 69.5; DB 1; Length 833;  
Best Local Similarity 23.7%; Pred. No. 34;  
Matches 31; Conservative 13; Mismatches 40; Indels 47; Gaps 6;

QY 37 NFKKTQALEQVTKYLEDFVNG--DHVILQKTVACLEF-----LREALISPFK 83  
DB 366 NVEBAAYTEDEGLHVNDSFLDGLNKEDALAKIVACLEEGCGQEKVYRLRWL-----FS 420  
QY 84 THEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPD-----HOTLSHR 124  
DB 421 RQRWGEPIPIIH-----W--EDGTSVAVPETELPVLPVTKDIRPSGTGSSPLANTL 470

QY 125 LPWAEGRNEDG 135  
DB 471 TDWLEVTREDDG 481

RESULT 15  
US-09-018-211-2  
Sequence 2, Application US/09018211  
Patent No. 6048716

GENERAL INFORMATION:  
APPLICANT: Lawlor, Elizabeth  
TITLE OF INVENTION: No. 6048716e1 Compounds  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA

COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018,211  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/844,086  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: 9607993.4  
FILING DATE: 18-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimm, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P31457-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 833 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-018-211-2

Query Match 9.6%; Score 69.5; DB 2; Length 833;  
Best Local Similarity 23.7%; Pred. No. 34;  
Matches 31; Conservative 13; Mismatches 40; Indels 47; Gaps 6;

QY 37 NFKKTQALEQVTKYLEDFVNG--DHVILQKTVACLEF-----LREALISPFK 83  
DB 366 NVEBAAYTEDEGLHVNDSFLDGLNKEDALAKIVACLEEGCGQEKVYRLRWL-----FS 420  
QY 84 THEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPD-----HOTLSHR 124  
DB 421 RQRWGEPIPIIH-----W--EDGTSVAVPETELPVLPVTKDIRPSGTGSSPLANTL 470  
QY 125 LPWAEGRNEDG 135  
DB 471 TDWLEVTREDDG 481

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Job time : 51 secs

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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:26:24 ; Search time 176 Seconds  
(without alignments)  
360.571 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725

Sequence: 1 AVTKPRYQMQRMTSSTL.....HQTLSRLPMAEGNRDGYL 137

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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	725	100.0	137	US-10-781-581-226	Sequence 226, App
2	725	100.0	660	US-10-311-034-26	Sequence 26, Appl
3	725	100.0	683	US-10-092-900A-342	Sequence 342, App
4	493	68.0	798	US-10-168-582-5	Sequence 5, Appli
5	493	68.0	798	US-10-979-095-5	Sequence 5, Appli
6	482	66.5	1192	US-10-764-330-1	Sequence 1, Appli
7	464	64.0	1339	US-10-082-830-282	Sequence 282, App
8	403.5	55.7	382	US-11-097-143-1725	Sequence 1725, Ap
9	382.5	52.8	316	US-10-042-894A-25	Sequence 25, Appl
10	145	20.0	71	US-10-029-386-29832	Sequence 29832, A
11	81.5	11.2	325	US-10-408-765A-1520	Sequence 1520, Ap
12	80.5	11.1	349	US-10-369-493-175	Sequence 175, App
13	79.5	11.0	248	US-11-096-568A-32990	Sequence 32990, A
14	79.5	11.0	300	US-11-096-568A-32989	Sequence 32989, A
15	79.5	11.0	330	US-11-096-568A-32988	Sequence 32988, A
16	79	10.9	422	US-11-188-298-12964	Sequence 12964, A
17	78	10.8	279	US-10-042-894A-10	Sequence 10, Appl
18	78	10.8	279	US-10-424-599-249309	Sequence 249309,
19	77	10.6	298	US-10-506-454-333	Sequence 333, App
20	76	10.5	496	US-10-767-701-43815	Sequence 43815, A
21	75.5	10.4	392	US-10-437-963-202651	Sequence 202651,
22	75.5	10.4	977	US-10-467-535-1	Sequence 51119, A
23	75	10.3	317	US-10-425-114-51119	Sequence 51119, A
24	75	10.3	455	US-10-425-114-42633	Sequence 42633, A
25	74	10.2	335	US-11-096-568A-24584	Sequence 24584, A
26	74	10.2	417	US-10-437-963-203451	Sequence 203451,
27	74	10.2	449	US-11-096-568A-24583	Sequence 24583, A

28	74	10.2	455	6	US-11-096-568A-24582	Sequence 24582, A
29	74	10.2	561	4	US-10-437-963-172520	Sequence 172520,
30	73.5	10.1	602	4	US-10-158-761-10462	Sequence 10462, A
31	73.5	10.1	634	5	US-10-739-930-6363	Sequence 6363, Ap
32	73	10.1	1371	4	US-10-437-963-183969	Sequence 183969,
33	72.5	10.0	240	4	US-10-283-122A-71183	Sequence 71183, A
34	72.5	10.0	362	4	US-10-283-122A-63450	Sequence 63450, A
35	72.5	10.0	767	6	US-11-079-463-8192	Sequence 8192, Ap
36	72	9.9	397	4	US-10-437-963-112279	Sequence 112279,
37	72	9.9	410	4	US-10-415-011-15	Sequence 15, Appl
38	72	9.9	467	4	US-10-362-774-3	Sequence 3, Appli
39	72	9.9	467	4	US-10-369-493-6071	Sequence 6071, Ap
40	72	9.9	606	4	US-10-156-761-13742	Sequence 13742, A
41	72	9.9	1325	4	US-10-437-963-182507	Sequence 182507,
42	71.5	9.9	636	4	US-10-389-586-1296	Sequence 1296, Ap
43	71.5	9.9	636	5	US-10-732-923-9642	Sequence 9642, Ap
44	71.5	9.9	2106	4	US-10-408-765A-2093	Sequence 2093, Ap
45	71	9.8	215	4	US-10-425-114-39157	Sequence 39157, A

## ALIGNMENTS

```
RESULT 1
US-10-781-581-226
; Sequence 226, Application US/10781581
; Publication No. US20050019746A1
; GENERAL INFORMATION:
; APPLICANT: Birk Therapeutics Ltd.
; APPLICANT: Seery, Liam
; APPLICANT: Hayes, Ian
; APPLICANT: Murphy, Finbarr
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
; FILE REFERENCE: 8912/2015
; CURRENT APPLICATION NUMBER: US/10/781,581
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 10/764,238
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/457,533
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: UK 0301566.6
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-581-226

Query Match      100.0%; Score 725; DB 5; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.1e-73;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRYQMQRMTSSTLGFRIEIKKAGTCNTNFKKQALBOYKVLDPVGDHV 60
DB 1 AVTKPRYQMQRMTSSTLGFRIEIKKAGTCNTNFKKQALBOYKVLDPVGDHV 60
QY 61 ILQKVVACLEIRALELISPFKTHEVVGSSILFVHDHTGLAKYWMIDFGKTVALLPDHQT 120
DB 61 ILQKVVACLEIRALELISPFKTHEVVGSSILFVHDHTGLAKYWMIDFGKTVALLPDHQT 120
QY 121 LSHRLPMAEGNRDGYL 137
DB 121 LSHRLPMAEGNRDGYL 137

RESULT 2
US-10-311-034-26
; Sequence 26, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
```

APPLICANT: YUE, Henry  
APPLICANT: LAL, Preeti  
APPLICANT: BANDMAN, Olga  
APPLICANT: BOROWSKY, Mark L.  
APPLICANT: AU-YOUNG, Janice  
APPLICANT: LU, Yan  
APPLICANT: GANDHI, Ameena R.  
APPLICANT: TRIBOULEY, Catherine M.  
APPLICANT: CHAWLA, Narinder K.  
APPLICANT: YAO, Monique G.  
APPLICANT: LU, Dzung Anna M.  
APPLICANT: GREENWALD, Sara R.  
APPLICANT: RAMKUMAR, Jayalaxmi  
APPLICANT: GRIFFIN, Jennifer A.  
APPLICANT: KEARNEY, Liam  
APPLICANT: BURFORD, Neil  
APPLICANT: NGUYEN, Daniel B.  
APPLICANT: TANG, Y. Tom  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: HE, Ann  
APPLICANT: THORNTON, Michael  
APPLICANT: HAPALIA, April  
APPLICANT: ARVIZU, Chandra S.  
APPLICANT: GURURAJAN, Rajagopal  
APPLICANT: LO, Terence P.  
APPLICANT: KHAH, Farrah A.  
APPLICANT: RECIPON, Shirley A.  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: POLICKY, Jennifer L.  
APPLICANT: DING, Li  
APPLICANT: GREYER, Megan  
APPLICANT: ELLIOTT, Vicki S.  
APPLICANT: THANGAVELU, Kavitha  
APPLICANT: BATRA, Sateev  
APPLICANT: ISON, Craig H.  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PI-0125 PCT  
CURRENT APPLICATION NUMBER: US/10/311.034  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
60/228,056  
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PERL Program  
SEQ ID NO 26  
LENGTH: 660  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023242A1 7480774CD1  
US-10-311-034-26

Query Match 100.0%; Score 725; DB 4; Length 660;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 60  
DB 508 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 567  
QY 61 ILQKYVACLEELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALLPDHQT 120  
DB 568 ILQKYVACLEELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALLPDHQT 627  
QY 121 LSHRLPWAEGNRDEGYL 137  
DB 628 LSHRLPWAEGNRDEGYL 644

RESULT 3  
US-10-092-900A-342

Sequence 342, Application US/10092900A  
Publication No. US20040043382A1  
GENERAL INFORMATION:  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Taupier Jr., Raymond J.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Li, Li  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Gusev, Vladimyr Y.  
APPLICANT: Ji, Weizhen  
APPLICANT: Gorman, Linda  
APPLICANT: Miller, Charles E.  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Patturajan, Meera  
APPLICANT: Gangoli, Baha A.  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Guo, Xiaojia Saaha  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Liu, Yi  
APPLICANT: Anderson, David W.  
APPLICANT: Spaderna, Steven K.  
APPLICANT: Catterton, Elina  
APPLICANT: Lette, Mario W.  
APPLICANT: Zhong, Haihong  
APPLICANT: Alsobrook, John P.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-290C  
CURRENT APPLICATION NUMBER: US/10/092.900A  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: USSN 60/274,322  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/283,675  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: USSN 60/338,092  
PRIOR FILING DATE: 2001-12-03  
PRIOR APPLICATION NUMBER: USSN 60/274,281  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/274,191  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/325,681  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: USSN 60/304,354  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: USSN 60/279,995  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: USSN 60/294,899  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: USSN 60/287,424  
PRIOR FILING DATE: 2001-04-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 768  
SEQ ID NO 342  
LENGTH: 683  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-092-900A-342

Query Match 100.0%; Score 725; DB 4; Length 683;  
Best Local Similarity 100.0%; Pred. No. 3.4e-72;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 60  
DB 531 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 590

QY 61 ILQKVVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 120  
DB 591 ILQKVVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 650  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 651 LSHRLPMAEGNREDGYL 667

## RESULT 4

US-10-168-582-5  
; Sequence 5, Application US/10168582  
; Publication No. US20040058426A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YANG, Junming  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: BURFORD, Neil  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Dyoung Aina M.  
; APPLICANT: REDDY, Roopa  
; APPLICANT: YUE, Henry  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LAI, Preeti  
; APPLICANT: KAHN, Farrah A.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0002 PCT  
; CURRENT APPLICATION NUMBER: US/10/168,582  
; CURRENT FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/177,731  
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PERL Program  
; SEQ ID NO 5  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040058426A1 2902460CD1  
US-10-168-582-5

Query Match 68.0%; Score 493; DB 4; Length 798;  
Best Local Similarity 67.9%; Pred. No. 5e-46;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKERYQWRETMSSSTLTGFRIGIKKADGTCNTNFKKTQALBOVTKVLEDVYDGDHV 60  
DB 642 AVTKERYQWRETMSSSTLTGFRIGIKKEDGTVNRDPKTKTRQVTEAFREFTKGNHN 701  
QY 61 ILQKVVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 120  
DB 702 ILIAYRDLKALRTITLSEVSPFKCHEVIGSSLLFTHDKKEQAKVMMIDFGKTVALLPDHQT 761  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 762 LQHDVPMQEGNREDGYL 778

## RESULT 5

US-10-979-095-5  
; Sequence 5, Application US/10979095  
; Publication No. US20060068481A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YANG, Junming  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: BURFORD, Neil  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Dyoung Aina M.  
; APPLICANT: REDDY, Roopa  
; APPLICANT: YUE, Henry

; APPLICANT: YAO, Monique G.  
; APPLICANT: LAI, Preeti  
; APPLICANT: KAHN, Farrah A.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0002 PCT  
; CURRENT APPLICATION NUMBER: US/10/979,095  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/10/168,582  
; PRIOR FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/177,731  
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PERL Program  
; SEQ ID NO 5  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 2902460CD1  
US-10-979-095-5

Query Match 68.0%; Score 493; DB 5; Length 798;  
Best Local Similarity 67.9%; Pred. No. 5e-46;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKERYQWRETMSSSTLTGFRIGIKKADGTCNTNFKKTQALBOVTKVLEDVYDGDHV 60  
DB 642 AVTKERYQWRETMSSSTLTGFRIGIKKEDGTVNRDPKTKTRQVTEAFREFTKGNHN 701  
QY 61 ILQKVVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 120  
DB 702 ILIAYRDLKALRTITLSEVSPFKCHEVIGSSLLFTHDKKEQAKVMMIDFGKTVALLPDHQT 761  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 762 LQHDVPMQEGNREDGYL 778

## RESULT 6

US-10-764-330-1  
; Sequence 1, Application US/10764330  
; Publication No. US20040265790A1  
; GENERAL INFORMATION:  
; APPLICANT: Cooke, Michael P.  
; APPLICANT: Sauter, Karsten  
; APPLICANT: Wiltshire, Tim  
; APPLICANT: Tarantino, Lisa  
; APPLICANT: Fletcher, Colin  
; APPLICANT: Wen, Ben  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING T LYMPHOCYTES  
; FILE REFERENCE: P10970S10  
; CURRENT APPLICATION NUMBER: US/10/764,330  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US 60/442,792  
; PRIOR FILING DATE: 2003-01-25  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-764-330-1

Query Match 66.5%; Score 482; DB 5; Length 1192;  
Best Local Similarity 67.2%; Pred. No. 1.5e-44;  
Matches 92; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 AVTKERYQWRETMSSSTLTGFRIGIKKADGTCNTNFKKTQALBOVTKVLEDVYDGDHV 60  
DB 869 AVTKERYQWRETMSSSTLTGFRIGIKKEDGTVNRDPKTKTRQVTEAFREFTKGNHN 928  
QY 61 ILQKVVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 120

Db 929 ILIAYRRLKAIKRAITLISPFKCHVYGSLLFTHDKKEQAKVMIDFGKTTPLPBGQT 988  
Qy 121 LSHRLPWAEGNREDGYL 137  
Db 989 LQHDVPWQEGNREDGYL 1005

RESULT 7  
US-10-082-830-282

; Sequence 282, Application US/10082830  
; Publication No. US20030077604A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Yongsang  
; APPLICANT: Recipon, Herve  
; APPLICANT: Salceda, Susana  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Turner, Leah  
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific  
; FILE REFERENCE: DEX-0249  
; CURRENT APPLICATION NUMBER: US/10/082,830  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 60/243,802  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 282  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 282  
; LENGTH: 1339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-830-282

Query Match 64.0%; Score 464; DB 4; Length 1339;  
Best Local Similarity 53.1%; Pred. No. 1,8e-42;  
Matches 93; Conservative 14; Mismatches 30; Indels 38; Gaps 1;

Qy 1 AVTKPRYQWREMTSSTLTGFRIGIK----- 28  
Db 1145 AVTKPRYQWREMTSSTLTGFRIGIKLRSANGALPTAPGSRPLHPLGPQVLPV 1204  
Qy 29 -----KADGCTNTEFKTQALEQVTKVLEDFVDDHYILQKYVACLEELREALEISPF 82  
Db 1205 LSKAATKEDGTVNDRPFKTKTREQVTEAFREFTKGNHILLAYVDRLKAITTLEVSPPF 1264  
Qy 83 KTHVVSLLFVHDHTGLAKVMMIDFGKTTALPDHQTSLRLPWAEGNREDGYL 137  
Db 1265 KCHVIGSSLLFTHDKKEQAKVMIDFGKTTPLPBGQTLQHDVPWQEGNREDGYL 1319

RESULT 8  
US-11-097-143-1725

; Sequence 1725, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 4308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1725  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-1725

Query Match 55.7%; Score 403.5; DB 6; Length 382;  
Best Local Similarity 56.9%; Pred. No. 2.2e-36;  
Matches 78; Conservative 19; Mismatches 39; Indels 1; Gaps 1;

Qy 1 AVTKPRYQWREMTSSTLTGFRIGIKADGCTNTEFKTQALEQVTKVLEDFVDDHY 60  
Db 196 AVTKPRYQWREMTSSTLTGFRIGIKSDGTSKDKFTTKSREQIKLAFLELSGPH 255  
Qy 61 ILQKYVACLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTTALPDHQT 120  
Db 256 ILPRYIORLRAIRATLAVSEFFQTHEVIGSSLLFVHDQTH-ASIMLIDFAKVELPPQLR 314  
Qy 121 LSHRLPWAEGNREDGYL 137  
Db 315 IDHYSANKVGNHEDGYL 331

RESULT 9  
US-10-042-894A-25

; Sequence 25, Application US/10042894A  
; Publication No. US2003009011A1  
; GENERAL INFORMATION:  
; APPLICANT: Shi, Jinrui  
; APPLICANT: Beach, Larry  
; APPLICANT: Wang, Hongyu  
; APPLICANT: Rafalecki, Antoni J.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: NO. US2003009011A1 Inositol Polyphosphate Kinase  
; FILE REFERENCE: 1286  
; CURRENT APPLICATION NUMBER: US/10/042,894A  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 60/261,465  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-042-894A-25

Query Match 52.8%; Score 382.5; DB 4; Length 316;  
Best Local Similarity 55.1%; Pred. No. 3.9e-34;  
Matches 75; Conservative 19; Mismatches 41; Indels 1; Gaps 1;

Qy 2 VTKPRYQWREMTSSTLTGFRIGIKADGCTNTEFKTQALEQVTKVLEDFVDDHY 61  
Db 149 VTKPRYQWREMTSSTLTGFRIGIKSDGTSKDKFTTKNRPQVLEAFDFVAGFPBV 208  
Qy 62 LQKYVACLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTTALPDHQT 121  
Db 209 IPKYINRLRAIRIDLVNSKEFTTHEVIGSSLLFVHDSKN-ANIMLIDFAKTLILPDIRI 267  
Qy 122 LSHRLPWAEGNREDGYL 137  
Db 268 NHTSEVYVGNHEDGYL 283

RESULT 10  
US-10-029-386-29832  
; Sequence 29832, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
; FILE REFERENCE: AEMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 29832  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR19.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.69  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.85  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
; OTHER INFORMATION: SWISSPROT HIT: P17105, EVALUATION 1.00e-27  
US-10-029-386-29832

Query Match 20.0%; Score 145; DB 4; Length 71;  
Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVTKRYMOWRMTSSTLGFRIKIX 28  
Db 44 AVTKRYMOWRMTSSTLGFRIKIX 71

RESULT 11  
US-10-408-765A-1520  
; Sequence 1520, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Boi D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088,465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1520  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1520

Query Match 11.2%; Score 81.5; DB 4; Length 325;  
Best Local Similarity 32.7%; Pred. No. 2.7;  
Matches 32; Conservative 7; Mismatches 26; Indels 33; Gaps 6;

Qy 6 RYMOWR-----ETWST--STLG-----FRLEGKAD-GTCNTNFKTKQALEQVTK 49  
Db 144 RYVMMRWGILMSYTWSTFGSGTIGNKRDTHTIEDLSLGHVCDT----- 190  
Qy 50 VLEDFVGDHYILQYVACLELRALHISPPFKTHEV 87

Db 191 -LLDFCDPDI--KFTQCLAEKELRLQETLHKFHEL 224

RESULT 12  
US-10-369-493-175  
; Sequence 175, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xiandeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 175  
; LENGTH: 349  
; TYPE: PRT  
; ORGANISM: Xenorhabdus nematophilus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(349)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-175

Query Match 11.1%; Score 80.5; DB 4; Length 349;  
Best Local Similarity 24.6%; Pred. No. 3.9;  
Matches 31; Conservative 16; Mismatches 60; Indels 19; Gaps 6;

Qy 14 MSSTLGFRIEGIKAD--GTCNTN-----FKTKQALEQVTKVLEDFVGDHYILQY 65  
Db 191 LSNEDTNFKFDYISRPLOCICNISLPMWELFCNDSTIELISPL-----GKTKQPSY 244  
Qy 66 VACLELRALHISPPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALLPDHQTLSRL 125  
Db 245 AALAHLEY-AGEEVPKVFQKHNIASSDIHKIFHTGAPMMW-DGFGKAVDADKM---HNI 299  
Qy 126 PMAEGN 131  
Db 300 GQKTGN 305

RESULT 13  
US-11-096-568A-32990  
; Sequence 32990, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 32990  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(248)  
; OTHER INFORMATION: Ceres Seq. ID no. 13601691  
US-11-096-568A-32990

Query Match 11.0%; Score 79.5; DB 6; Length 248;  
Best Local Similarity 20.5%; Pred. No. 3.2;  
Matches 31; Conservative 31; Mismatches 44; Indels 45; Gaps 5;

```

QY      11 RETMSSTLGFRIEIGIKKADGTCNTNFKGTQALQGVTKVEDPVDGDHVLQKTYA--- 67
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      71 KDRQTTVSLGFRVSGFKIPDHQESSFWRAEKL-----VLGYMNDGARTLAKRTVSSMS 125
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      68 -----CIEELREALEISPEFKTHEVY---GSLLFVHDHTGL----- 101
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      126 PADSNLTFCNCAFASEVYGGCNGILAQLELTKMDFEQTLYHFNCSILIMTYENESILMQG 185
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      102 -----AKYWMIDFGKTV---ALPDHQT 121
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      186 GDDAPAPRAQVLYDFAHVLDGNGVIDHNFL 216
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

RESULT 14
US-11-096-568A-32989
; Sequence 32989, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2/750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32989
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(300)
; OTHER INFORMATION: Ceres Seq. ID no. 13601690
US-11-096-568A-32989

```

[illegible][illegible]

Search completed: May 21, 2006, 04:30:06  
Job time : 177 secs



```
Publication No. US2006008828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Disease Nucleic Acids
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4059
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 2511
; OTHER INFORMATION: Xaa = Pro or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 2981
; OTHER INFORMATION: Arg or Gln
; US-10-501-834-6

Query Match          9.0%; Score 65; DB 6; Length 4059;
Best Local Similarity 24.1%; Pred. No. 34;
Matches 36; Conservative 21; Mismatches 51; Indels 48; Gaps 8;

Qy      9 QWRRTMSTSLGRIEIKKADGTCNTNFK-----KQALQGYTK----- 49
Db      2459 RWEIITSTYVNF--DNCVAIRTCSCFGQGGYTKTKQLKRVSSNVAEPHPAA 2516
Qy      50 VLEDF-----VDDGDIYLOKYVACLEELREALISPPFK--THEVVGSSLLFVHDHTG 100
Db      2517 VLEDDGSLGSKNSHYL-----ASMETLSPTCLTNASFSQIVGSGVGEAVLTHRMISA 2571
Qy      101 LAKYWMIDFKTVALPD-----HQTLSHRLPW 127
Db      2572 LAN--SLDVPKRLITTDISNKTITVNYVEDTLSNYGW 2607

RESULT 3
US-10-510-162-4
; Sequence 4, Application US/10510162
; Publication No. US20060099580A1
; GENERAL INFORMATION:
; APPLICANT: Corena T. McMANUS
; APPLICANT: David A. JONES
; TITLE OF INVENTION: METHYL-CPG BINDING DOMAIN PROTEIN 2 HOMOLOGS
; FILE REFERENCE: 38509-0016US1
; CURRENT APPLICATION NUMBER: US/10/510,162
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/US03/10631
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/369,851
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-510-162-4

Query Match          8.8%; Score 64; DB 6; Length 194;
Best Local Similarity 25.3%; Pred. No. 0.71;
Matches 25; Conservative 20; Mismatches 36; Indels 18; Gaps 6;
```

```
Qy      6 RYMQWRETMSSTSLG--RIEIGIK--KADGTCNTNFKKQALQGYT-----KVLEDFV 55
Db      51 RYMQWESLEKPPQVQWGRLOGLQAVSSAGELSTLDLANTLQKLVPSYTGSLLEDLA 110
Qy      56 DG-DHYILOKYVACLEELREALISPPFKTHEVVGSSLL 93
Db      111 SGLEHSCPMPLACSS---DAVEIIP---AEGVGISQL 142

RESULT 4
US-10-525-621-1
; Sequence 1, Application US/10525621
; Publication No. US20060100418A1
; GENERAL INFORMATION:
; APPLICANT: Kiyosue, Yuko
; APPLICANT: Sasaki, Hiroyuki
; APPLICANT: Teukita, Shoichiro
; APPLICANT: Eisai Co., Ltd.
; TITLE OF INVENTION: CULTURED XENOPUS LAEVIS CELL LINES
; FILE REFERENCE: 082368-00240US
; CURRENT APPLICATION NUMBER: US/10/525,621
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: PCT/JP03/10434
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: JP 2002-241487
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2829
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-10-525-621-1

Query Match          8.6%; Score 62; DB 6; Length 2829;
Best Local Similarity 24.2%; Pred. No. 48;
Matches 24; Conservative 16; Mismatches 43; Indels 16; Gaps 2;

Qy      5 PRYQWRETMSSTSLGRIEIGIKAD-----GTCNTNFKKQALQGYT 49
Db      2553 PRYSTWRTSSSSILASSESSSEKASEDEKQVCSFPGPRSECSSAGTKRKIXESB 2612
Qy      50 VLEDFVDDGDIYLOKYVACLEELREALISPPFKTHEV 87
Db      2613 ILTTPNSGSSSTIAESNCSELSFKTLVYQMAPAYSKTBDV 2651

RESULT 5
US-10-706-435A-26
; Sequence 26, Application US/10706435A
; Publication No. US20060088547A1
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Lanar, David E.
; APPLICANT: Hillier, Collette J.
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Kumar, Sanjay
; APPLICANT: Rogers, William
; APPLICANT: Barbosa, Arnoldo
; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
; FILE REFERENCE: 003/285/SAP
; CURRENT APPLICATION NUMBER: US/10/706,435A
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,719
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word XP
; SEQ ID NO 26
; LENGTH: 456
; TYPE: PRT
```





```
Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: N1 et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: FP469P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-246-999-49
```

```
Query Match      8.1%; Score 59; DB 7; Length 700;
Best Local Similarity 25.6%; Pred. No. 17;
Matches 21; Conservative 13; Mismatches 42; Indels 6; Gaps 3;
```

```
QY      28 KKADGTCTNFKTQALAEQVTVLEDFVGDHV--IIQKY---VACLEELREALISPPF 82
DB      173 RKDGLCFPPDPKRRQVGPASNVYLGQMEDYKVGISRKHKMCLCVQEVWSGLR-QPVS 231
QY      83 KTHEVVGSSLLFVHDHTGLAV 104
DB      232 AVHSGDGSRLFILEKEGYVKI 253
```

```
RESULT 9
US-11-146-700-1
; Sequence 1, Application US/11/146700
; Publication No. US20060094100A1
; GENERAL INFORMATION:
; APPLICANT: Columbia University
; APPLICANT: Jogi, Gerwald
; TITLE OF INVENTION: STRUCTURAL MODELS OF CARINITINE
; FILE REFERENCE: 070050.2801
; CURRENT APPLICATION NUMBER: US/11/146,700
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: PCT/US04/00170
; PRIOR FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: 60/438,172
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-146-700-1
```

```
Query Match      8.1%; Score 58.5; DB 7; Length 626;
Best Local Similarity 21.6%; Pred. No. 16;
Matches 40; Conservative 21; Mismatches 55; Indels 69; Gaps 10;
```

```
QY      4 KRYWQWRETMSTSTLGF-----IIEGKKADGTCTNFKKTQAL 44
DB      104 KTAIVLQFPQPVVITYSSPVLTPKQDVEDVLOGQLRPAKALIEGV-----LDFK--SMI 153
```

```
QY      45 EQVTVLEDFVGDHVIIQKYVACLEELREALISP-----FPK-----THEVVGSSL 92
DB      154 DNEETLPEV-FLGGQFLCMNQYQILSSCR---EVPKQDSVNFLLSKSRPFHITVNVY 209
QY      93 LF-----VHDHTS-----LAKVMIDFGKTVALPDHOTLSRLPMAEG----- 130
DB      210 QFELDVTYVHDGTPLTSDQIFVQLEKIWNSSLIQSNKEPVGILTSNHRMTWAKAYNNLIKD 269
QY      131 --NRE 133
DB      270 KVNRE 274
```

```
RESULT 10
US-10-511-937-2968
; Sequence 2968, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: FRY, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2968
; LENGTH: 1866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2968
```

```
Query Match      8.1%; Score 58.5; DB 6; Length 1866;
Best Local Similarity 20.3%; Pred. No. 73;
Matches 30; Conservative 20; Mismatches 39; Indels 59; Gaps 6;
```

```
QY      26 GIKKADGTCTNFKTQALAEQVTVLEDFVD-----GDHVIIQKYVA 67
DB      119 GLKRPHOSCGSSPPKCKQQLLELAKKYLQLTSAQRYRSQIPSGQPHAFHYVVP 178
QY      68 CLEELREA-----LEISPFKTHEVVGSSLLFVHDHTGLAKW 105
DB      179 PI--LRRTATSLDTPPEGALMGDVKEADVDISLDFNTRVNRKSPRYTVLLGKAGM----- 232
QY      106 MIDFGKTVALPDHOTLSRL--PWAEGN 131
DB      233 ----GKT-----TLAHLCCQWAEGR 249
```

```
RESULT 11
US-11-264-784-63
; Sequence 63, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
```

```

; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL136 USA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 63
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Candida albicans (GenBank Accession No. EAL04510)
US-11-264-784-63

Query Match
Best Local Similarity 23.9%; Score 58; DB 7; Length 353;
Matches 21; Conservative 16; Mismatches 21; Indels 30; Gaps 7;

QY 50 VLEDFVDDGVHVLQKY--VACLEELREALISPPFK-----THEVVGSSLLFVHDHT 99
DB 245 VFNSTF---HSLMFTYFSLSLCK-----IRVNFPRKRLITMQITQFVGSIALIHSP- 295
QY 100 GLAKVMIDFGKTVLAPDHQTLSHRLPW 127
DB 296 ----VWIDTSHVLS-PDN-----LKN 312

RESULT 12
US-10-505-928-519
; Sequence 519, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 519
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-519

Query Match
Best Local Similarity 7.9%; Score 57.5; DB 6; Length 192;
Matches 26; Conservative 23; Mismatches 45; Indels 9; Gaps 4;

QY 8 MOWETMSSTSTLGFRIEIGIKADGTC---NTNFKTQALBQVTKVLEDF---VDG-DHV 60
DB 33 LKFNIEFVTVPTTIGTNEKIKLNGTAKGISCHFTWDVGCGKAPKIMKSYRCIDGIIV 92
QY 61 ILQKTVACLEELREALISPPFKTHEVVGSSLLFVHDHTGLAK 103
DB 93 VDSVDVRLERAK--TEIAKTKFAENGSTPLVIANKQDLPK 133

RESULT 13
US-10-505-928-209
; Sequence 209, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
```

```

; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 209
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-209

Query Match
Best Local Similarity 7.7%; Score 56; DB 6; Length 288;
Matches 31; Conservative 15; Mismatches 43; Indels 38; Gaps 8;

QY 10 WRETMSSTSTLGFRI-BGIRKADGTCNTNFKTQALBQVTKVLEDFVDGSHVLQKYVAC 68
DB 16 WEECFQAAVQALAGQIIRXALTBKRVSTKSAADLVET-----DHLVEDLIIS- 67
QY 69 LEELREALISPPFKTHEV-----GSSLLFVHDHTGLAKVMIDFGKTVLAPDHQTL 121
DB 68 --ELRER-----PFSHRFIAEAAAGKACVLTHTSP-----WITD-----PIDGTC 107
QY 122 S--HRLP 126
DB 108 NFVHRFP 114

RESULT 14
US-10-706-435A-4
; Sequence 4, Application US/10706435A
; Publication No. US20060088547A1
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Lanar, David E.
; APPLICANT: Hillier, Collette J.
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Kumar, Sanjai
; APPLICANT: Rogers, William
; APPLICANT: Barbosa, Arnaldo
; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmidum
; FILE REFERENCE: 003/285/SAP
; CURRENT APPLICATION NUMBER: US/10/706,435A
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,719
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word XP
; SEQ ID NO: 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: LSA-NRC(H)Mut
US-10-706-435A-4

Query Match
Best Local Similarity 7.7%; Score 56; DB 6; Length 457;
Matches 26; Conservative 16; Mismatches 27; Indels 26; Gaps 4;

QY 23 RIRGIRKADGTCNTNF-----KKTQALBQVTKVLEDFV-----DGDHVLQ 63
DB 369 KIRGKRYEKTKYKNNFPPNDKSLYDEHIKKYKNDQVNEKEKFKIKSLFHFPGDNLQ 428
QY 64 KYVACLEELREALISPPFKTHEVVGSSLLFVHDH 98
DB 429 ----IYDELSIEDITYFM--KLGGSGSGFHHHH 456

RESULT 15
US-10-511-937-2929
; Sequence 2929, Application US/10511937
```

```

; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2929
; LENGTH: 1842
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2929

```

```

Query Match          7.7%; Score 56; DB 6; Length 1842;
Best Local Similarity 27.7%; Pred. No. 1.4e+02;
Matches 28; Conservative 16; Mismatches 29; Indels 28; Gaps 8;

Qy 38 FKKTOA----LEQVTKVLEDFV---DGDHVILO-KYVACLEBRLREALEISPF----FKT 84
    ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|:
Db 860 FKKQECRDILLPVTTKEIKELBQKQDMQHQVLERKY--CVELNLSILEVLSYQDAFTY 917
    ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|:

Qy 85 HEV--VGSSILFVHDHTGLAKVMMIDFGKTVALLPDPHQTLSH 123
    ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|:
Db 918 HHIOEIWQLRLRTVNRT-----VITWGR-----DHILISH 947
    ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|:

```

Search completed: May 21, 2006, 04:30:20  
 Job time : 9 secs